SEO	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	rucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			IRKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
1			EFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR
1			FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
	Į.		
5906	146	2038	PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
3306	140	2038	REGAGSGRNASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
Į.			PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
1			DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
i i		1	A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
			HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
1	I		DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVFK
1			TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
1	Į.		KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
	ł		QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
1	1	l	TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
1	1	l	SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN
1	1	I	ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
i		l	DEDUCTION OF THE PROPERTY OF THE PARTY OF TH
		l	DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
		l	VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY
			SGIGSMONEQLSDSFPYEFFQV
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
1	I		KATSKVPSAPHFVHPNDHAMREAELKKKWVEEMREKOOAAREOE
1	I		ROKERTIESYCODVLERGEEFEHKEEVLGELMMFPGLDDEATRK
			AYYKEFRKVVEYSDVILEVLDARDPLGCRCPQMEEAVLRAQGNK
1			VI MI MI METEL MENDERHAMME DAT DATA DATA DATA DATA DATA
1	l		KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL
1			NRCSVPVDQASESLLKSKACFGAENLMRVLGNYCRLGEVRTHIR
1			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF
1			IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
1			NLEEISNYYGVSGFQFTEHFLTAVAHRLGKKKKGGLYSQEQAAK
1	l .		AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
1			EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI
1			ENKTTYYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
			MAKITYTKIGDDIGICIMPAKAQPGWAKKAVDHRPKSNSMVDVC
	1		SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
			SDSMMSALDLSGNADDGVGD
5908	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
1			HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
			GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
			VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT
1			WCCCCPDCOVACCORDS & DOCUDA CTURO TOWARD OF MARRIES
1			VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEBCK VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	
1 2202		5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
1 1			SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
			CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
			STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
1 1			ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
1			SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
1 1			DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK
1			
1			IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
			GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
1			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSRAPE
	1		SSESWKPEQLGEGSVPDRPGNQSIELSRPAREAAVITEAGDQGM
1		J	VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE
] [		ļ	DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG
1		ļ	EGRLQLRASVKRKSRPCSLPVSELBTVIASACGDPETPRTHYIR
1 1		}	THE THOMPS COOKS A THE PASSED IN THE ACCOUNT FOR THE PROPERTY IR
1 1			IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
1 1			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
1			HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
	1		SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
1 1			EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
1			SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT
			IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR
1	1		
			RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence ·	_	\=possible nucleotide insertion)
			GGGGSDSEARSSQSSLDLRREGSLSPVNSQKITLLLQSPAVKFI
1			TNPEFFTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYOH
			NRDLVNFINMFADTRLELPRGWEIKTDQQGKSFFVDHNSRATTF
	1	Į.	IDPRIPLONGRLPNHLTHROHLORLRSYSAGEASEVSRNRGASL
		1	LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFLROPNIFEMLOE
			ROPSLARNHTLREKIHYIRTEGNHGLEKLSCDADLVILLSLFEE
1			BIMSYVPLQAAFHPGYSFSPRCSPCSSPQNSPGLQRASARAPSP
			YRRDFEAKLRNFYRKLEAKGFGQGPGKIKLIIRRDHLLEGTFNQ
			VMAYSRKELQRNKLYVTFVGEBGLDYSGPSRBFFFLLSQELFNP
			YYGLFEYSANDTYTVQISPMSAFVENHLEWFRFSGRILG\LALT
1			HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDESFHQSLQW
			MKDNWITDILDLTFTVNBEVFGQVTERELKSGGANTOVTEKNKK
l l			BYIERMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVFDARELE
			LVIAGTAEIDLNDWRNNTEYRGGYHDGHLVIRWFWAAVERFNNE
			QRLRLLQFVTGTSSVPYEGFAAPPWEPMGLRRFLP*KKWGKITS
			LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT
5910	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLEVLKTNYGIPSACFSOPPT
			AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP
1			IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTITSFYAVC
1			FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL
			LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL
			RGAQLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF
1			ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH
i			LLILETFLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRWM
			AWTMKGCCTH
5911	109	595	QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF
1	1		CGHRRGGAAFKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS
1			GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET
			GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
5912	924	277	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP
1			SGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN
			TAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI
			CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ
			VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHWGAEIPTTL
5913	46	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS
1			DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS
			HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN
1			FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE
1			SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM
	Į.		E*/DDQEVIKPENGRHQDSTLKEDVPEQGKDDVREVKVRQNSEP
1			CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT
1			YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI
			AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED
5914	960	124	NLGGSELPPERALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN
1			ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG
1			GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS
			IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE
1			SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP
	1		KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH
			PHRHLPGLCRPAATS
5915	1604	703	FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA
			PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT
	i i		POEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS
1			KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS
			PRELPGSEFSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS
-			PVLQELPGPAGGEFPEGL**AAGPAAH
. 5916	256	633	SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR
			TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH
			PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA
5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptid
ID	beginning	nucleotide	(AsAlanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVD
			FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLEKAYFRNAGN
			HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
5918	13	1247	BGAQVARRRSRRQWRAGRCGRGRGGRRAERTGGRGPPGRPRPL
	ļ	Į.	PGPARRGRRMETPFYGDEALSGLGGGASGSGGTFASPGRT.PP
			APPTAAAGSMMKKDALTLSLSEQVAAALKPAPAFASYPPA\AD
	ł		APSAAPPDGLLASPDLGLLKLASPELERLIIQSNGLVTTTPTS
		ì	QFLYPKVAASEEQEFAEGFVKALEDLI:KQNQLGAGRAAAAAA
			AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRG
			RGGAAT\VAPAAEPVPFPPPPPPPGALGPRRP/RLALOGRRPOT
	1		PDVP\SPGESP\PLSPIET\DTPRRI\KAKRKRL\RNPOIRAP
			PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQL
			QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVQGDSQGTPTSSQGSINMEHWISQAIHGSTTSTTSSSSTQS
	l	l .	GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIOVERPOGS
		İ	GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRP
			LREFFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTN
			PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRS
			KVAYSILHKLGTKOEPMVRPGDRVALVFPNNDPAAFMAAFYGC
			LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHK
			LPKSPTGEIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDA
			NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEA
			TIVNVLDFKKDVGLWHGILTSVMNMMHVISIPYSLMKVNPLSW
			QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVAD
			ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRP
			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMP
			AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKN*
			FEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLM
			VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIV:
			VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLI
			KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPRQK
1			PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLS
			VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRAEKIAVM1
			MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHI
			QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVI
			TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAG
			KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGFVLWCL
J			SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEI
1			CTKGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTQSFSKI
- 1			FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALF
			HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSF
- 1	J		LGEIWVHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTQTIWAR
	ļ		TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPII
- 1	ļ		TETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQRALDLVPLV
- 1			TNVVLEEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ
5920	1381		LDPIYVAYNM
3720	1381	1499	QLGAVAHAGVSRIPP*LFPPLHPTFLSLWCLHHKLP/HPPGASN
- 1			VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGF
			SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM
			LAAAPLHEQKOMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
			LLMLKSPESLHAKIDBAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKFMDAFTGSGLKRKFDDVDV
	j		GSSVSNSDDEISSSDSADSCDSLNPFTTASFTPTSILKRQKQLR
- 1		1	RKWVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
ĺ	1		LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
	ĺ		GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR
			IDABEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD
			RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
	į		Q\GAAQQPQ\*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG
1922	2475	495	AAATHLIILRVIENRGAEGKRK

SEO   Predicted   Predicted end   Amino acid segment containing signs   ID   beginning   mucleotide   (A-Alanine, C-Cysteine, D-Aspartic   No: nucleotide   location   Columnic Acid, F-Phenyialanine, C-Cysteiden, I-Robert   Corresponding   H-Histidine, I-Robert   Corresponding   H-Histidine, I-Robert   Corresponding   Corresponding	Acid. E-
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G=G location corresponding H=Histidine, I=Isoleucine, K=Lysine	
location   corresponding   H=Histidine, I=Isoleucine, K=Lysine	lvcine.
corresponding to first L=Leucine, M=Methionine, N=Asparagi	ne,
to first amino acid P=Proline, Q=Glutamine, R=Arginine,	
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown	
	, *=Stop
	on,
sequence   \mpossible nucleotide insertion    CLYMATQYKVCSPRNDRPDACYNPSEPAATTVFEI	D mov T v down
SKIITRTBEKEIPKQITLRFDACAINSKKLEIGO	RTGLLLGDT
RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDS	UST ONGES
PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINR	ATTOMORMA
LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKN	TELOTARM
IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAP	DTIPT*KAE
ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNCIG	
TIT**DLNHTEKNPFSKFSKLKTA*AHAESH*DWT	
RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMSEL	LGFSVYASR
EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSW	GYR/TP/VY
MLNWIIRLQAILEIISNETGRALTVLANQETQMRN	AIYQNRLAL
DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVR	OMTKLAHVP
IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIR	CLLLPCVL
PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQR	DRKREDESE
5923 137 638 QLCGRRGQRFRTSTKRMHPI*RTCPNTNL/IILLS	NAME OF PART
QQENRELWISLEEHQDALELIMSKYRKQMLQLMVA	SENIOI KOP
LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQ	ECKTOEKLA
QLELENKELRELLSISSESLOARKENSMDTASOAT	K
5924 274 2146 EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLMSL	PPTSVRRM
PLITTVILLKNVARHHMKLLCSKAFSTQLQQKIFL	
SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTI	
HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKL	KITKTIQNG
RELFESSLCGDLLNEVQASE\Q*NQSIESRKEKRK	KSNKHDSSR
SEERKSHKIPKLEPEBONRPNERVDTVSEKPREEP	LKEGSPSS
ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYFWWP: EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVRE	MARSONDE
LLABATKQASNHSEKQKIRKPRPQRERAQWDIGIA	KRICHKOYEE
REERIEQYTFIYIDKQPEBALSQAKKSVASKTEVK	TPPPPQUI.
NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEE	PPPVKIAW
KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQ	
DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPN	
VSSPEATSGSTGSVEKKQCRRSIRTRSESEKSTEV	PKKKIKKE
5925 216 1911 MMTARGPRATGLODGARGEVICTURED PROPERTY	
	MWGQDSTL
QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKEI	CHOWLRPE
INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSO DLELDLSGQQVPGQVHGPEMLARGMVFLDPVQESSS	EEAVILLE
QSHPKHSSRKPRLLQSRALPAAHI PAPPHEGSPRDQ	
ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNF	
PQGGENRNENESTSKAETSEDSASRGETTGRSQKE	
GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGE	RGPREKGK
GLGRSFSLSSNFTTPREVPTGTKSHRCDECGKCFTF	SSSLIRKK
IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTG	EKPHECNE
CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQS	SD/LTKHQ
RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKF	
S926 2 233 DRCLMLKQGSQFGSPPAT/CEPPAPPVYQAPCQSCF	
SDSPHHTPVHPPPEHSAACPAPATCCPPPRSMS	EFFGAMEP
5927 4146 1248 KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPA	AKVGTDT.2
YKKYGDKKLHEKKPLQKHKQAHOTPEKRVNTGEERR	
KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLER	
WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYE	HYHAIFDO
MQQQRAEDNEAKWKRE1YGRGLPERQKGQLAVERAK	QVEEFLQR
KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGK	PRNKEEEV
YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQ	EGSEEADM
RRKK\IBSLKAHANARAAVLKEQLERKRKEAYEREK	KAMEBHTA
AKGVKSSDVSPPLGQHRTGGSPSKQQMRSVISVTSA	
SLIDTRETSEEMQKINNAISSKRRILRRINENLKAQ	
LSDTFEINVHEDAKKHEKEKSVSSDRKKWEAGGQLV DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSV	
DISFSTERMI VGEV I RIGFNGSPRRANGASPIDSV	DELLIGERE

SEO	Predicted	I Bur 32 ab 3 a - 3	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		_	LOLOTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
			AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
1	Į.	1	GTNKDB\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1	1		HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1			HERBY POVOSVQCSPERSPAPRSHEPPRNKNKNSLLTGLSTG
1	i		LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
1			EDENIKEGPSDSEDIVFESTDTDLQELQASMEQLLREQPGERYS
1			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
1	Į.		GEIASECECDSVFNHLBELRLHLEQEMGFEKFFEVYRKIKAIHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVWADGAYQEDNDE
5928	4145	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
			KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
	ļ.		WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
1			MOOORAEDNEAKWKREIYGRGLPEROKGQLAVERAKQVEEFLOR
			KREAMONKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
			YLARI.RQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
	l		RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
	f		
i			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
			SLTDTRETSBEMOKTNNAISSKREILRRLNENLKAQEDEKGKON
			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLK1LGEAE
			LOLOTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1			AIVDSPVETKSPEFSEAS POMSLKLEGNLEEPDDLETEILOEPS
1			GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
ĺ	ĺ		VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
			EDENIKEGPSDSEDIVFBETDTDLQELQASMEQLLREOPGEEYS
			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
			GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKATHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5929	3	1558	DEDENTELCSKIVQNIEGNEHQHEYAKIEGHEVMADGAYQEDNDE
3323	3	1220	LDFSNTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
1			LTPVSREBALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
			WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
1			AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
1 1			KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI
1			LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
			RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
1 1			QLDSHFSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK
1 1			LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAFDGLHTVE
1 1	j		GRYYLCICTLLKCKTTNLNTCGDSABTASTRFEMFSLSGTFGTQ
1 1	ļ		YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGR
1	J		LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSK
5930	113	6082	RGNCFWIVPFTMAORTGLEDPERYLFVDRAVIYNFATOADWTAX
1		5002	
1 1			KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
1 1			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRGM
I	ì		LODREDOSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
1			IPGE\LERQLLQAMPILESFGNARTVQNDNSSRFGKFIRINFDV
1			TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
			KSDLLLEGFWNYRFLSNGYIPIPGO\QDKGNFRGDPGEAMHIMG
1	İ		FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAOKL
			CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
1 1		Į.	KATYERLFRWLVHRINKALDRTKRQCASFIGILDIAGFEIFELN
	1		CEPOT CINCERPLY OF SECURITY PORTIONS
1 1			SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
1			DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVBKLVQEQ
1			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
1	1		NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
	1		KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
			LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP

SEO	Predicted	I management and an a	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
10:		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline. O=Glutamine D=Arminine
	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W Tomber to M To
ţ	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\mpossible nuclectide insertion)
			NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
1	1		LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
			NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEBLLKVK
		ı	BKQTKVEGELEEMERKHQQLLEEKNILAEQIQAETELFAEAEEM
			BAQI KARGEDERARKINQQIDEEKNILAEQIQAETELFAKAEEM
			RARLAAKKQELEEILHDLESRVEEBEERNQILQNEKKKMQAHIQ
1		ł .	DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
			IKEKKLMEDRIAECSSQLAEREEKAKNLAKIRNKQEVMISDLEE
ſ	í	ſ	RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLOL
Į.			AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
1			EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
1			OF THE PER PERSON AND ADDRESS OF A PARTY OF THE PERSON AND ADDRESS OF A PARTY OF THE PERSON AND ADDRESS OF A PARTY OF A P
	i		QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
1		ì	FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
1	1		QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK
1		l	FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
1			ECQEEEEBARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
			KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
1			HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
	1		VPTVALCIADAL TRALTANTON TO THE PROPERTY OF THE
			KETKALSLARALEBALEAKEBFERQNKQLRADMEDLMSSKDDVG
1			KNVHELEKSKRALEQQV\EEMRTQLEELEDBLQATEDAKLRLEV
	1		NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
			RALAVASKKKMEIDLKDLEAQIBAANKARDEVIKQLRKLQAQMK
			DYQRELEEARASRDEIFAQSKESEKKLKSLEARILQLQEELASS
í			ERARRHAEGERDELADEITNSASGKSALLDEKRRLEARIAGLEE
			SLEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
			COLEDONAL NAME OF THE PROPERTY
			QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
1			QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
			NARMKQLKRQLEBABBEATRANASRRKLQRELDDATEANEGLSR
			NARMKQLKRQLEBAEBBATRANASRRKLQRELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
			NARMKQLKRQLEBABBEATRANASRRKLQRELDDATEANEGLSR
5931	113	6082	MARMKQLKRQLEBABBBATRANASRRKLQRELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNBTQPPQSE
5931	113	6082	NARMKOLKROLBERAEBEATRANASRRKLORELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNBTOPFOGSE RGNCFWIVPFTMAORTGLEDPERYLFVDRAVIYNPATGADWTAK
5931	113	6082	NARNKOLKROLEBRABEATTANNASRRKLORELDDATEANEGI,SR EVSTLKNILBRGGISFSSSRSGRRQLHLEGSSLELSDDTESK TSDVNETOP PQSE RGNCPHITPFTMAGRTGLEDPERYLFVDRAVINNBATQADMTAK KLWHISSRHOFBAASIKEBRODEVNVELAENGKKAWNNDDIO
5931	113	6082	MARMYQLKRQLERAEBRYTRANASRRKIQRELDDATEANGGLSR LYSTLKMELMGGJISSSSSSGRQLHLEGGASLELSODDTESK TSDVMETQFQGE RGGCFFTUFFTHAGRTGLEDPERTIFFDRAVIYMPATQADWTAK KLWNIPSERNGFRAASIKERRODEVNVELAEMGKKAMYNKODIQ MMPPKFSKPUEMABLTCLMERAVULHILDRYYSGLIFTYSGLIFTYSGLF
5931	113	6082	MARMOLISQUEGASEBATRANASRIKUGRELDATEANEGLER EVSTLÄNLERKOGTISTSSISSGRIGHLEGASLELSDDDTESK TSDWIBTOPFOSE RONCFHIVPFTRAGRICLEDPERVLFFURRAVIYNDATOADWITAK KLIWIFSBERHOFEARSIKBERGDEWWIELABMKKEARWIKDDIO MANDPKESKVERMBELTCLMEASVLENLEDKYSGLITYTSGIF CVULNDYKNIKJISSMITEMTKEKREBENDEHTVLISESAYRCH
5931	113	6082	MARKOLTROLERABEARTANASRRIORELDDATEANEGLES EVETLINBLERGED/ISFOSSESSERRICHERASELESDOTESK TSD/MISTOPPOSE KONCFHIPPITAGRITULEDDERILFFORAVITAPATOLATTAK KLWHISBERGERAASIKERRODEVWELABROKKAMMINDDIO KMPPPKFSKEWEMAELCILENSEVELHUNGERVSGULTVYSELF CVVINVYNILFITSBITTIGERGEKEKERDPHITAISSSAYRCH LOREROSELICHBESGARKTENTKYNIVOTTAHVASSEKRORDH
5931	113	6082	MARKOLTROLERABERATEMANGRIKORELDATEMANGLISE EVETLINKLIENDOT STESSESSORGILHEGISLELESDOTESK TSONWITOPOGE TSONWITOPOGE EVENLYFINARATURENDE STESSESSORGILHEGISLELESDOTESK ENCHTI PEPINARATURENDE STESSESSORGILHEGISLELESDOTESK ENCHT PEPINARATURENDE STESSESSORGILHEGISLELESDOTESK ENCHT PEPINARATURENDE STESSESSORGILHEGISLENGENDE STESSESSORGILHEGISCHE STESSESSORGIL
5931	113	6082	MARKICJEROLERABERATRANASREKJORELDDATEANEGLISR EVETLIFIKLERODJETSESSSSGERGLILBERISLELSDODTESK TSDINISTOPPOSE  ROCKFITTP-FITAGRETULEDDEFILFFORAVITEPATOLITYTEK KLIVITI-SBERIGFERALSCHEBERIJ-FORAVITEPATOLITYTEK KLIVITI-SBERIGFERALSCHEBERIJ-FORAVITERABIOKEAMWINDDIG KLIVITI-SBERIGFERALSCHEBERIJ-FORAVITERABIOKEAMWINDDIG COVINSYTNI-PITSBITI-SBERIGFERALSCHEBINFPITI'A ISSSAYECK LOREDOS-LICITOSSGAGATETSTIKVOTYLAHVASSFROKETERIT-TILBEROLLGANFTLESFORARTVODDISSFROKETERIT-TILBEROLLGANFT-TILBEROLLGAN
5931	113	6082	MARKOLTROLERABERATEMANDRIKORELDATEMANGLISE EVETLINKLIENDOTES ESSESSIOCHLIEGALELES EDDOTES K TSDWITTOPOGE ENGLEFT FINAGE TÜLEDERE LI FVDRAVITHERATOADHTAK KLIVHI SERNIGE AMSI IKERKODEVAVIELABDIGKAMANNODIO MARPPERSVENERABALICURISAS ZIENIKORVYSGLIST VITYSEIF LOGIBLOGIST LI GENERALICURISAS ZIENIKORVYSGLIST VITYSEIF LOGIBLOGIST LOGISTA LI GENERALICURISAS ZIENIKORVYSGLIST VITYSEIF TÜRE LEBOLLADINDITES ERFONER FYRONDISSERBOTH TI LIGOTY TOYI VARMIETYLLEKSRAVEOKNOEFFFHI TYOLLISI AGEHL SEDLLLESFERMERYLSSKYIET FIROQUOKKNIPSODIERAMIN M
5931	113	6082	MARKOLTROLERABERATEMANDRIKORELDATEMANGLISE EVETLINKLIENDOTES ESSESSIOCHLIEGALELES EDDOTES K TSDWITTOPOGE ENGLEFT FINAGE TÜLEDERE LI FVDRAVITHERATOADHTAK KLIVHI SERNIGE AMSI IKERKODEVAVIELABDIGKAMANNODIO MARPPERSVENERABALICURISAS ZIENIKORVYSGLIST VITYSEIF LOGIBLOGIST LI GENERALICURISAS ZIENIKORVYSGLIST VITYSEIF LOGIBLOGIST LOGISTA LI GENERALICURISAS ZIENIKORVYSGLIST VITYSEIF TÜRE LEBOLLADINDITES ERFONER FYRONDISSERBOTH TI LIGOTY TOYI VARMIETYLLEKSRAVEOKNOEFFFHI TYOLLISI AGEHL SEDLLLESFERMERYLSSKYIET FIROQUOKKNIPSODIERAMIN M
5931	113	6082	MARKICJEROLERABERATEANARREKJORELDATEANEGI.SR  EVETLINBLIENDOT JESSESSSREGKLIEGAS-LELSDOTESK TSD/MISTOPPOSE  ROKOFFUTP-FINAGETULEDDERTLI-FORAVUTRAPT-GLATTAK KLWHI-SBERGERAAS-IKERSODEWWELABROKEAMWINDDIO KAMPPAFKSKUEMBAELTCULESS-LUHLLOCRY-SGG-LUTY-TYSEI-F COVINDYNINI-PTSENTIGESGAGHTETINKTOKUTY-LAWAS-BROKEAMWIND- LORREDO-ELDGESGAGHTETINKTOKUTY-LAWAS-BROKEAMWIND- TIPGS-LUEROLL-GAHTILESFONART/VOJDINSSRFOKFIETINFOU- TOTY-URAMI ETILLESFANAFOA-GROKEFTEI-FOLLGS-LOSEH- ESDLLLBOFFRIYER-SINGTI FI FOGY-ODKONFROD-DORAMHIMS ESDLLLBOFFRIYER-SINGTI FI FOGY-ODKONFROD-DORAMHIMS ESDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ESDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ESDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ESDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ESDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ESDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ENDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ENDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ENDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ENDELLBOFFRIYER-SINGTI FOGY-ODKONFROD-DORAMHIMS ENDELLBOFFRIYER-SINGTI FOGY-DORAMHIMS ENDELLBOFFRIY-FOGY-DORAMHIMS ENDELLBOFFRIY-FOGY-DORAMHIMS ENDELLBOFFRIY-FOGY-DORAMHIMS ENDELLBOFFRIY-FOGY-FOGY-FOGY-FOGY-FOGY-FOGY-FOGY-FOG
5931	113	6082	MARKOLTROLERABERATEANARRICORELDATEANEGISR EVETLINILERAGOTISTESSASSAGULHIRGALERISDOTESK TSÖNMITÖDFÖGE RÖNGFÄTTPFINAGRITÜLEDPERTLFVÖRAVITHERATÖLDITÄK KLÜMI SERNÖFERAGITEDPERTLFÖRENLÖRITYSGLITYTSELF RÖNGFÄTTPFINAGRITÜLEDPERTLFÖRENLÖRITYSGLITYTSELF RÖNGFÄTTPFINAGRITÜLEDPERTLFÖRENLÖRITYSGLITYTSELF RÖNGFÄTTPRIAGRITÜLERINGENLÖRITYSGLITYTSELF RÖNGFÄTTRÖLITISSELI BATTRÖKKEREMPIPATIN ISSSAYROK TÖRBÜR KLÖNGFÄTTRÖLITÄTTRÖLITYTSELF TÖRBÜLERINGENLÖRITYSELTYTÖLLÖRITÄKERÖN TÖRTÄNDELTERFÖRENTÖLDITÄKERÖN TÖRTÄNDELTERFÖRENTÖLDITÄKERÖN TÖRTÄNDELTERÄTÄKERÖN FÖRBERTÄNDITÄKERÖN FÖRBERTÄNDITÄKER FÖRBERTÄR FÖRBERTÄNDITÄKER FÖRBERTÄR FÖ
5931	223	6082	MARKOLTROLERA BERATAMANGERIO (RELIDATENTICI.SE EVETLINILILARIO) TESCHISCHOGILLIRICA, LEUS ELDOTEK I TSTUMENTO POGIS E EVETLINILILARIO TESCHISCHOGILLIRICA, LEUS ELDOTEK I TSTUMENTO POGIS EL CONTROLERA EL CANTO DE LEUS EL CANTO DE L'EL C
5931	113	6082	MARKOLTROLERABEARTANARGRICORELDATEANEGISR EVETLINHLERODTESSKSSRONGGLHERGISLERSDOTESK TSDWIRTOPOGES ROCKPHITPETHAGRITULEDPERTLEVETAVITHERATGADITAK KLVMI SERNOFENAGRITULEDPERTLEVETAVITHERATGADITAK KLVMI SERNOFENAGRITULEDPERTLEVETAVITHERATGADITAK KLVMI SERNOFENAGLICULENSAVITHAUKORITUGIL KLVMI SERNOFENAGLICULENSAVITHAUKORITUGIL LOSEDGE LICHEGEGARATERIK KOVI OLIMANSER ORTERIARI LOSEDGE LICHEGEGARATERIK KOVI OLIMANSER ORTERIARI NOVI VANNIETULESGARATERIK KOVI OLIMANSER ORTERIARI NOVI VANNIETULESGARATERIK KOVI OLIMANSER ORTERIARI FSHEELISMIKAVOS VIQORITS FRIERROTIO DAMPERTVOQUIL LOSEDGE LICHEGERIKOTIST FOR DELIGIORE DELIGIORI LICHEGERICAL KATUELLERIKAVIS VISOROFICA DELIGIORI DIAPPERTVOQUIL LATUELLERIKAVIRINIA LOPERGARS FIGURE LOPETERIA KATUELLERIKAVIRINIA LOPETERIARI DELIGIORI SERGENITO DELIGIORI PER PROPERTIONI
5931	223	6082	MARKOLTROLERABERATEMANGRETORELDATEMATGLISE EVETLINILLERODT STEGRSSRONGLILLEROLERES DOTTEK TSÖNNETÜD ROGE EVETLINILLERODT STEGRSSRONGLILLEROLERES DOTTEK TSÖNNETÜD ROGE EVELLERITEMAN EVETLISTERETE PUDAN TÜRÜNTQADUTAN KÜNETÜT PURAN EVETLISTERETE PUDAN TÜRÜNTÇADUTAN KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR KÜNETÜR TÜRÜN LEROLLIANDE VILINLER KÜNETÜR TÜRÜN LEROLLIANDE LER PORAN TÜNÜNDIS SERÖNTE TÜR TÜN TÜRÜN LEROLLIANDET LER PORAN TÜNÜN ÖNKORTIFBE TÜR LIFDY TÜRÜN LEROLLIANDET LER PORAN TÜNÜN ÖNKORTIFBE TÜR LIFDY TÜRÜN LEROLLIANDET LER PORAN TÜNÜN ÖNKORTIFBE TÜR LIFDY TÜRÜN LEROLLIANDET LER PORAN TÜNÜN ÖNKORTIFBE TÜR LIFDY TÜRÜN LEROLLIANDET LER PORAN TÜNÜN ÖNKORTIFBE TÜR LIFDY TÜRÜN LEROLLIANDET LIBORT TÜR LÜNÜN ÖNKORTIFBE TÜR KÜNÜN TÜRÜR LEROLLIANDET LIBORT TÜR TÜR ÜNÜN ÖNKORTIFBE TÜR ÜNÜN TÜRÜR LÜRÜN ÜN ÜN ÖNKORTIFBE TÜR ÜNÜN ÖNKORTIFBE TÜR TÜRÜN ÜN ÖNKORTIFTÄN ÜN ÖNKORTIFBE TÜR TÜRÜN ÜN ÖNKORTIFTÄN ÜN ÖNKORTIFBE TÜR TÜRÜN ÖNKORTIFTÄN ÜN ÖNKORTIFBE TÜR TÜRÜN ÖNKORTIFTÄN ÜN ÖNKORTIFBE TÜR TÜRÜN ÖNKORTIFTÄN ÜN ÖNKORTIFTÄN ÜN ÖNKORTIFBE TÜR TÜRÜN ÖNKORTIFTÄN ÜN ÖNKORTIFTÄN ÖNKORTIT
5931	223	6082	MARKOLTROLERABERATEANARGRICORELDATEANEGISR EVETLINHLEROODTISSSSSSSSSSSCHLERGISLEISEDDETEK TSDWIRTOPROSE RONCPHITPETRAGRITULEDPERTLEVORATTYPEATGADITAK KLVMITSBERROPERAGRITULEDPERTLEVORATTYPEATGADITAK KLVMITSBERROPERAGRITULEDPERTLEVORATTYPEATGADITAK KLVMITSBERROPERAGRITULEDPERTLEVORATTYPEATGADITAK KLVMITSBERROPERAGRITULEDERTULEVORATIONAL KLVMITSBERROPERAGRITULENDERTULEVORATIONAL LOREDOELLOREGORAGHTERINKOUN (D'LAMANSHERMENDEN LOREDOELLOREGORAGHTERINKOUN (D'LAMANSHERMENDEN LOREDOELLOREGORAGHTERINKOUN (D'LAMANSHERMENDEN LOREDOELLOREGORAGHTERINKOUN (D'LAMANSHERMENDEN FSHEELLSMLKUWSSVLJORGTSPHEERNED)ARGRITULENDE FSHEELLSMLKUWSSVLJORGTSPHEERNED ARGRITULENDE FSHEELLSMLKUWSSVLJORGTSPHEERNED ARGRITULE LAMANSHERMENSON'E IF DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN (DELEGEN PERAGRITULE LAMANSHERMENSON'E IN DELEGEN PERAGRITULE LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERMEN LAMANSHERM
5931	113	6082	MARKOLTROLERABERATEMANGRETIORELDATEMATIGLES EVETLINELIBEROD IS SESSESSEGULHERIGALERIDOTES EVETLINELIBEROD TES EVETLINELIBEROD
5931	123	6082	MARKICJEROLERABERATEANAGREKORELDATEANEGISR EVETLINILARDODTESSKSSROGREGHLEGGISLEISDOTESK TSDWIRTOPROSE ROCKPHTPPTRAGRETGLEDPERTLFYDRAVITHPATGADITAK KLWHI SBERGIF BAASIKERRODEWAVELABOKKEAWANDOLO KENPPERSKEVERMAGLECURASAVILANDORTUSTUTTYSSEF CVVINYTOLIPITSENII BINTREKKEREMPPHIVA ISSSAVECK UVINYTOLIPITSENII BINTREKKEREMPHIVA ISSSAVECK TOVINYTOLIPITSENII BINTREKKEREMPHIVA ISSAVECK TOVINYTOLIPITSENII BINTREKKEREMPHIVA ILDEGEN TOPATE ISSAVECK TOVINYTOLIPITSENII BINTREKKEREMPHIVA ILDEGEN TOPATE INTERNITY TOVINYTOLIPITSENII BINTREKKEREMPHIVA ILDEGEN TOPATE INTERNITY TOVINYTOLIPITSENII BINTREKKEREMPHIVA ILDEGEN TOPATE TOPATE INTERNITY TOVINYTOLIPITSENII BINTREKKEREMPHIVA ILDEGEN TOPATE TOPATE INTERNITY TOVINYTOLIPITSENII BINTREKKEREMEN TOPATE TOPATE INTERNITY TOPATE TOPA
5931	113	6082	MARKOLTROLERABERATEANARRICORELDATEANEGLISE  VESTILINALIBRODI ISSESSISSISSICALILBRIGALERISEDOTESK  TSÖNNETÖPPÖGE  RÖNCHFÜTPFYTRÄGRETÜLEDPER ELFYÜRAVITREPATÖADITÄK  KLIVALI SERNIGERAASI KERRÖDEVWELLABIOKEAWANNODIO  RÖNCHFÜTPFYTRÄGRETÜLEDPER ELFYÜRAVITREPATÖADITÄK  KLIVALI SERNIGERAASI KERRÖDEVWELLABIOKEAWANNODIO  LOORBOGASI LOTORSGAARTENTIKUVI OYLANYASIEKORKONE  TORVILDEVIALIP YESEKI LIRWALVI OYLANYASIEKORKONE  TORVILDEVIALIPE YESEKI LIRWALVI OYLANYASIEKORKONE  TORVILDEVIALIPE LIRVARVOODISKERKORT ELFYD  FERBELLESMIKAVOSVIJORGIS FRIKERNTDASAPBENTYAQLI  KANTERLENIKAVIRINGALDETKROGASF TOLI LIRVARVET  KANTERLENIKAVIRINGALDETKROGASF TOLI LIRVARVET  GERBEROKEP DALORIAN ELFERTORIOONISKATIONIST VICTORIANIST TOLI ONI
5931	173	6082	MARKOLTROLERABERATEANARRICORELDATEANEGLISE  VESTILINALIBRODI ISSESSISSISSICALILBRIGALERISEDOTESK  TSÖNNETÖPPÖGE  RÖNCHFÜTPFYTRÄGRETÜLEDPER ELFYÜRAVITREPATÖADITÄK  KLIVALI SERNIGERAASI KERRÖDEVWELLABIOKEAWANNODIO  RÖNCHFÜTPFYTRÄGRETÜLEDPER ELFYÜRAVITREPATÖADITÄK  KLIVALI SERNIGERAASI KERRÖDEVWELLABIOKEAWANNODIO  LOORBOGASI LOTORSGAARTENTIKUVI OYLANYASIEKORKONE  TORVILDEVIALIP YESEKI LIRWALVI OYLANYASIEKORKONE  TORVILDEVIALIPE YESEKI LIRWALVI OYLANYASIEKORKONE  TORVILDEVIALIPE LIRVARVOODISKERKORT ELFYD  FERBELLESMIKAVOSVIJORGIS FRIKERNTDASAPBENTYAQLI  KANTERLENIKAVIRINGALDETKROGASF TOLI LIRVARVET  KANTERLENIKAVIRINGALDETKROGASF TOLI LIRVARVET  GERBEROKEP DALORIAN ELFERTORIOONISKATIONIST VICTORIANIST TOLI ONI
5931	113	6082	MARKOLTROLERA SERRIFAMANGERICORELDATEANEGLES EVETLINILLEROPO TESCHSER GEROLHEROLS LES ELDOTES EVETLINILLEROPO TESCHSER GEROLHEROLS LES ELDOTES EVETLINILLEROPO TESCHSER GEROLHEROLS LES ELDOTES EVETLINICATION TO THE SERVICE TO THE TESCH TESCHSER TO THE TES
5931	223	6082	MARKOLTROLERABERATEMANGRIKORELDATEMANGLISE  EVETLIKHALIBADOT ISTOSSASSAGULHURGALELESDOTESK TSÖNNITÖPPÖGE  RÖNCJETÜPPTIKAGETÜLEDERELIFÜDRAVITHERATGADITAK KLIVALI SBENGERAASI KRERKODEVVIELABIOKEAMANNODIO  RÖNCJETÜPPTIKAGETÜLEDERELIFÜPÜLENGKYTSÖLLTYTSÖLF  LÖNEROGELASI KRERKODEVVIELABIOKEAMANNODIO  LÖNEROGELASI KRERKODEVVIELABIOKEAMANNODIO  LÖNEROGELASI KRERKODEVVIELABIOKEAMANNODIO  LÖNEROGELASI KRERKODEVVIELABIOKEAMANNODIO  LÖNEROGELASI KRERKODEVVIELABIOKEAMAN SERGINDONI  TOYL IVANI ETYLLEKSAR AVOANDERTPELTYOLLISCI AGEHL  FSHEBILLEMIKAVUSSVLÖGENI SPKKERNTÖDASKPENTYAGILI  LÄVETERLEMIKAVUSSVLÖGENI SPKKERNTÖDASKPENTYAGILI  KATVERLERIKUMENINGELÖFTRÖGASF TÖLLE LAGPETERIN  KANTIFATUR ÖLLER FÖLLENDEN FÖLLEN FÖLLENDEN FÖLLE LAGPETERIN  KRÖMFRYTÖGLIVERSLIKKUM TLENDEN VACLI TENDENAGAL  KRÖMFRYTÖR TÖLLER FÖLLENDEN VACLI TENDENAGAL  KRÖMFRYTÖR TÖLLER FÖLLENDEN VACLI TENDENAGAL  KRÖMFRYTÖR TÖLLER FÖLLENDEN VACLI TENDEN VACLI TENDEN VACLI TENDENAGAL  KRÖMFRYTÖR TÖLLER FÖLLENDEN VACLI TENDENAGAL  KRÖMFRYTÖR TÖLLER FÖLLENDEN VACLI TENDEN VACLI T
5931	223	6082	MARKICLEGUERABERATEMANGREGOREUDATEMANGLISE  TSÖNMETÜD FÖGE  RÜCHT INFERDOTTSGESSKORGULHEGISLEELEGDOTEK  TSÖNMETÜD FÖGE  RÜCHT INFERDOTTSGESSKORGULHEGISLEELEGDOTEK  TSÖNMETÜD FÖGE  RÜCHT INFERDOTTSGESSKORGULHEGISLEELEGDOTEK  KRIPPER KREINER ALTEREENDE VILLEGUERABERDE SINGE  KINDPER KREINER ALTEREENDE VILLEGUERABERDE SINGE  KINDPER KREINER SINGER SINGERER EN PER VILLEGUERABERDE SINGER  LODERDOS ILCTOESSGARTENTIKKT OYLANVAS SHKORKORN  TORT LERGELIGHET SINGER FER DE KREINT POLLSS'LADERH  LODERDOS ILCTOESSGARTENTIKKT OYLANVAS SHKORKORN  TORT LERGELIGHET SINGER FER DE KREINT POLLSS'LADERH  LODERDOS ILCTOESSGARTENTIKKT OYLANVAS SHKORKORN  TORT LERGELIGHET SINGER FER DE KREINT POLLSS'LADERH  KREINTENTENT SINGER FER DE KREINT POLLSS'LADERH  KREINTENT SINGER SINGER FOR SINGER FER SINGER FER SINGER  CHILAGROWER FER ALT FER FER KREINT DARER FER VILLEGUER  GEBIER KRUPPER FER LET FER FER KREINT DARER FER VILLEGUER  GEBIER KRUPPER FER LET FER FER KREINT DE SEN SINGER FER SINGER F
5931	113	6082	MARKICLERGEARBEARTANARGREGORGUDATEANEGUSE  EVETLINALIBERGOT ETSESSESSEGGELHEGGALEELEGDOTESK  TSÖNNETÜDFÖGE  RÖNGFÄTTPFTRÄGRETÜLEDERETLFYDRAVITREPATÇADATAK  KLIVHI SERNIGERAASITERERGDEVVATELABDIGKAMANNODIG  RÖNGFÄTTPFTRÄGRETÜLEDERETLFYDRAVITREPATÇADATAK  KLIVHI SERNIGERAASITERERGDEVVATELABDIGKAMANNODIG  AURPPERSYNETÜRAMALICULERSAVELENLÖKTYSGULTYTSSEF  LÖNEBOGELLGTESSEALABTRÜKKELEDATPÄTNI LESSAVEKUM  LÖNEBOGELLGTESSEALABTRÜKKELEDATPÄTNI LESSAVEKUM  TÖRG LESGLÖLADATELESFORMETORONISSERGENTE TELTÖT  TÖYT VARMIETYLLEKSRAVEONADERTPEHTYÖLLSÜ AUSEHL  FSHEBILLBAMKAVOSVÜ,GENISFKERENTÖDASMEBENTYAGLI  LENTERLEMLKAVUSSVÜ,GENISFKERENTÖDASMEBENTYAGLI  LENTERLEMLKAVUSSVÜ,GENISFKERENTÖDASMEBENTYAGLI  LENTERLERGLÄVHRINKALDETKRGASFTGLICH LAGPETFELI  BURGULTÜLLERRANDENTALDETKRGASFTGLICH LAGPETFELI  LÖNGFÜLLLERRANDENTALDEBENOPPERTÄTTFVEKLOGIG  GESKERKERFRÖLGURAPHET LENGERTÖNETTVEKLOGIG  DIAGNETÜLLERRANDENTALDEBENOPPERTÄTTTVEKLOGIG  ENGERKRÖKERGURADAPETLI HENGERTÖNETTENTTVEKLOGIG  DIAGNETÜLLERRANDENTALDBERGENET TÄLDERGRÄCH  NATIKLAGSBERVABLINUTÜRI TVOLLOUTVETETARGSAYET  NATIKARGSBERVABLINUTÜRI TVOLLOUTVETETARGSAYET  NATIKARGANDEN AURPERTÄTELEDEN TÄLDERGRÄCHENTÖRE  NATIKARGANDEN AURPERTÄTELEDEN TÄLDERGRÄCHTÜRE  NATIKARGANDEN TÜLT FÖRMENDEN TÄLBERGANTERELLIKUN  REGONTVÖRGELERBERTÜRÜLLERGEN LARGEGLANDERLIKUN  REGONTVÖRGELERBERTÜRÜLLERGEN LARGEGLANDERLIKUN
5931	123	6082	MARKICLEROLERABERATEMANGRETICHELDATEMATGLISS  EVETLINHLIENDOT STESSESSORGHLIERGISLERSDOTTESK TSÖNWETOP GEGE  EVETLINHLIENDOT STESSESSORGHLIERGISLERSDOTTESK TSÖNWETOP GEGE  EVETLINHLIENDOT STESSESSORGHLIERGISLERSDOTTESK TSÖNWETOP GEGET  EVETLISSESSORGHLIERGISLER DER TE FFODAVITHENTOADNTAK  ENNEPPERVIERBAGELT LIERGESVIER LENGENGELAMMINGDED  ENNEPPERVIERBAGELT LIERGESVIER LIERGESVIERBENDHILMA ISSENVECH  LOGREDOS ILCTICESGLARTENTIKKVI OYLANYASSEKKORKDIEN  TORY LVEGAL LIERGESVIERBENDHILMA ISSENVECH  LOGREDOS ILCTICESGLARTENTIKKVI OYLANYASSEKKORKDIEN  TORY LVEGAL LIERGESVIERBENDHILMA ISSENVECH  LOGREDOS ILCTICESGLARTENTIKKVI OYLANYASSEKKORKDIEN  TORY LVEGAL LIERGESVIERBENDHILMA ISSENVECH  TORY LVEGAL LIERGESVIERBENDHILMA ISSENVECH  TORY LVEGAL LIERGESVIERBENDHILMA ISSENVECH  TORY LIERGESVIERBENDHILMA ISSENVECH  TORY LIERGESVIERBENDHILMA ISSENVECH  TORY LIERGESVIERBENDHILMA ISSENVECH  GESISKRYREPOLANDENDELT LIERGESVIERBENDHILMA  GESISKRYREPOLANDENDELT LIERGESVIERBENDHILMA  KOMMETTVOGLIVERSILVERMATIENTINDHIVELI IPHIKKRAGAK  KOMMETTVOGLIVERSILVERMATIENTINDHIVELI IPHIKKR
5931	113	6082	MARKICLERGUERABERATEANARGERIGGEEDDATEANEGUSE  EVETTLINGHLERGOTESTESSESSESSEGGLEHEGGLEEGEDOTEST  TSDWITTOPOGE  RECOFFITYPHEAGETTLEDPERTLYPDRAVITEPATCHATTAK  KLIVHI SERNIGFERASITEEDEETLYPDRAVITEPATCHATTAK  KLIVHI SERNIGFERASITEEDEETLYPDRAVITEPATCHATTAK  KLIVHI SERNIGFERASITEEDEETLYPDRAVITEPATCHATTAK  KLIVHI SERNIGFERASITEETLYPDRAVITERASITEEDEETLYN SESSAYROK  MARPPERTENDLYTESSELIEGENTOONDOORDOORDOORDOORDOORDOORDOORDOORDOORD
5931	113	6082	MARKICLEROLERABERATEMANGERICORELDATEMEGISE  FUSTLINILIBRODI JESOSSISSISSICALIBROSILERISOLESIS EUSTILIBRILIBRODI JESOSSISSISSICALIBROSILERISOLESIS EUSTILIBRILIBRODI JESOSSISSISSICALIBROSILERISOLESIS EUSTILIBRILIBRODI JESOSSISSISSICALIBROSICALIANINODIO  RECCUPITI PERPITARA TERROLEVAVILLABICERAMINODIO  RECCUPITI PERPITARA TERROLEVAVILLABICERAMINODIO  LOCREDOS ILCTOSSICALIBROSICALIBROSILERIS PORTIVA ILEGENAVICA  LOCREDOS ILCTOSSICALIBROSICALIBROSILERIS PORTIVA ILEGENAVICA  LOCREDOS ILCTOSSICALIBRO
5931	223	6082	MARKICLEROLERABERATEMANGERICORELDATEMANGLISE  EVETLINMLERIOD TESGESSIORGICHIEGOLERICOLEROLTER  EVETLINMLERIOD TESGESSIORGICHIEGOLERICOLEROLTER  EVETLINMLERIOD TESGESSIORGICHIEGOLERICOLEROLTER  EVETLINMLERIOD TESGESSIORGICHIEGOLERICOLEROLTER  ENDITERENTERABETEREROLTERICOLEROLTERICOLEROLTERICOLERO  ENDEPSENVERMAELICULUS VILINLERY VIGILIATURA SHERRICOLERO  ENDEPSENVERMAELICULUS VILINLERY VIGILIATURA SHERRICOLERO  LOCREDOS LICTOESGGARTENTIKKY LOYLARVAS SHERRICOLERO  TORI VILEGOLEROLTERICOLEROLTERICOLEROLTERICOLERO  TORI VILEGOLEROLTERICOLEROLTERICOLEROLTERICOLERO  TORI VILINDEN TESSESIORI TESTESIORI SHERRICOLEROLTERICOLERO  TORI VILINDEN TESSESIORI SHERRICOLEROLTERICOLERO  TORI VILINDEN TESSESIORI SHERRICOLEROLTERICOLERO  TORI VILINDEN TESSESIORI SHERRICOLEROLTERICOLERO  TORI VILINDEN TESSESIORI SHERRICOLERO  CHILARROMETE TRAILITERICOLEROLTERICOLERO  SERBELLISMLE VILINDEN TESSESIORI SHERRICOLERO  ENTERNICATION TORI SHERRICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLEROLTERICOLEROLTERICOLEROLTERICOLEROLTERICOLERO  GERBERGEROLTERICOLERO
5931	113	6082	MARKICLEROLERA SERRETANIAGERICORELDATEANEGLES  EVETLINIALIBADO TESCHISCORE GILHEGUSLELES DOTES  TESTINISTO POGE  EVETLINIALIBADO TESCHISCORE GILHEGUSLELES DOTES  TESTINISTO POGE  EVETLINIALIBADO TESCHISCORE GILHEGUSLELES DOTES  TESTINISTO POGE  EVETLINIA SERVEN PERA SETEREDO TESTINIALISTO TESTIN
5931	113	6082	MARKICJEROLERABBERTHANDERFRICHBELDATEANEGLES  EVETJIHMILBEROD ISSESSESSEGGLHEGGISLESSEDDTESK TSOWERDOPGES  EVETJIHMILBEROD ISSESSESSEGGLHEGGISLESSEDDTESK TSOWERDOPGES  ERCHETTPFFRAGRETGLEDERETLFVDRAVITHEATGARTAK KLWILDSBENGFBAASIKERBRODEVWELABERGEAMMINDOID  ERCHETTPFFRAGRETGLEDEREN FRAGRETGLEMMINDOID  EVETJIHMINDOID  FRAGRETGLESSEGGETENTKUTYLYTAMASSERGREDWEL  LODERDOSILCTGESGGARTENTKUTYLYTAMASSERGREDWEL  TUGY LEGALIESTYLESSETIESTYLTYCHDISSERGRET FILTFOT  TUGY LEGALIESTYLESSETIESTYLTYCHDISSERGRET FILTFOT  TUGY LEGALIESTYLESSESTET FOR GENERODASREPENTYAGLI  ESBELLLESMIKWYSSVLOPENTSFRENDENTSFRE
5931	113	6082	MARKICLEROLERABERATEMANGERICORELDATEMANGLISE  EVENTLINGHLEROOP JESGESSEGSEGGLHEROLERESEDDTESE  TEXTURDITUDE OPEN  EVENTLINGHLEROOP JESGESSEGSEGGLHEROLERESEDDTESE  TEXTURDITUDE OPEN  EVENTLINGHLEROOP JESGESSEGSEGGLHEROLERESEDDTESE  TEXTURDITUDE OPEN  EVENTLINGHLEROOP JESGESSEGSEGSEGSEGSEGSEGSEGSEGSEGSEGSEGSE
5931	113	6082	MARKICLEROLERABBERTANNAGRRICHBELDATEANEGLISE  EVETTLINGLIBERODT ESGESSSORGHLIBEGISLEELEDDTESK TSDINGTOPOGE  RECVEFT PFPTRAGRETGLEDPER EL FYDRAVITREPATCHATTAK KLIVHI SBERGER AAS I KRERKODE VWELLABUGGLAWATNOD IQ  RECVEFT PFPTRAGRETGLEDPER EL FYDRAVITREPATCHATTAK KLIVHI SBERGER AAS I KRERKODE VWELLABUGGLAWATNOD IQ  FOR STANDARD EL FORDER EL FORDER EL FORDER EL FORDER LODREDOS LICTIOSS GARTTETTEVI IQ VLANTAS SERGORDOR  TOYI IVANI ETYLLEKSRAVEOANDERFEL FYDLISSI ADEHL LODREDOS LICTIOSS GARTTETTEVI IQ VLANTAS SERGORDOR  TOYI IVANI ETYLLEKSRAVEOANDERFEL FYDLISSI ADEHL SEDLLLESSFRAVERSSOVI EL FORDER FSHEELLSMLKUVSSVLOGENI SFRERENTDOLSKEPRETY EL FORDER FSHEELLSMLKUVSSVLOGENI SFRERENTDOLSKAPERTYAGLI LEHLAMHAVES FALLET LICPHE IVENG LOGGS I GELEGRAFITM FSHEELLSMLKUVSSVLOGENI SFRERENTDOLSKAPERTYAGLI LATTEBELTRILDHE INFORMENT LICHGES I GELEGRAFITHE I FORDER LENGEN STROMENT LICHGE I FORDER I FORDER TENEN FSTEDLLISMLKUVSSVLOGENI SFRERENTDOLSKAPERTYAGLI LATTEBELTRILDHE I FORDER I FORDER I FORDER TENEN FSTEDLLISMLKUVSSVLOGENI SFRERENTDOLSKAPERTYROGLI CHARAGRETER LICHGE I FORDER I FORDER I FORDER TENEN NAVILLAGENDE VANDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER I FORDER I FORDER I FORDER I FORDER LENGEN FORDER I FORDER FORDER I FORDER FORDER I FORDER LENGEN FORDER FORDER I FORDER I FORDER FORDER I FORDER FORDER LENGEN FORDER FORDER FORDER I FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER FORDER
5931	223	6082	MARKICLEROLERABERATEMANGERICORELDATEMEGLISE  VESTALINALIBADO TSEGSSISSISSICALILBIOLISELES DOTES  TSÖNMETÜD ROGE  RÜNGERT PEPTHÄÄRETLÄBERETLE PUDAN TÄRINTÖADUTAK  RÜNGERT PEPTHÄÄRETLÄBERETLE PUDAN TÄRINTÖADUTAK  KONCERT PEPTHÄÄRETLÄBERETLE PUDAN TÄRINTÖADUTAK  KONCERT PEPTHÄÄRETLÄBERETLE PUDAN TÄRINTÖADUTAK  KONCERT PEPTHÄÄRETLÄBERETLÄBERETLÄBERETLÄBERAD  KONCERT PERTÄRETLÄBER TÄRINTÖRERETLÄBERAD  KONCERTÄRET PERSENTET ET RETEKTÄRETLÄBERAD  TÄRINTÄRETLÄBERAD  VESTALIBALIKAVSSI JORGET SERVERENTTYÖLLISSI, ÄÄSEHL  TÄRINTÄRETLÄBLIKAVSSI JORGET SERVERENTYÖLÄSERETTYÄRÖL  TÄRINTÄRETLÄBERAD  VESTALIBALIKAVSSI JORGET SERVERENTYÖLÄSERETTYÄRÖL  TÄRINTÄRETLÄBELATAVSSI TÄRINTÖN  TÄRINTÄRI LÄBELATAVASSI JORGET SERVERENTYÖLÄSERETTYÄRÖL  JORGET LÄBERAN ETÄNATÄN TÄRINTÄRETLÄBERAD  KANTELLERABIKAVSSI JORGET SERVERENTYÖLÄSERETTYÄRÖL  JORGET LÄBERAN ETÄNÄN TÄRINTÄRINTÄRET LÄBERAD  KANTELLERABIKAVSSI JORGET SERVERENTYÖLÄSERETTÄRÄ  SERÖLCINTYNISKÄOLIPHINTE ILLÖGET ORSET SERVER  LÖPETLÄLESERAN ETÄNÄN TÄRINTÄRET LÄBERAD  KANTELLISSERAN ETÄNÄN TÄRINTÄRINTÄRINTÄRINTÄRINTÄRINTÄRINTÄRIN
5931	113	6082	MARKICLERGUERABERATEANARGERICOREUDATEANEGUSE  EVETTLINGUERADOT ESTESSISSISSICIALHEGISLEELESDOTESI TSÖNNETÜPEÖGE  RÖNCHET VEPTIKAGE TÜLEDERE ELFVÜRAVITHERATGADITAK KÜMTI SERNIGFERASITERERGDEWWIELABIOKEAMINDOID  RÖNCHET VEPTIKAGE TÜLEDERE ELFVÜRAVITHERATGADITAK KÜMTI SERNIGFERASITERERGDEWWIELABIOKEAMINDOID  RÖNCHET VEPTIKAGE TÜLEDERE ELFVÜRAVITHERATGADITAK KÜMTI SERNIGFERASITERERGÜERWIELABIOKEAMINDOID  LOOBROGELICTIGSSIGABITERTERVI VI ÜLEN ÜLE BERGENETIT  TÜLT VARAHETYLLEKSRAVEONKOERTPELITYÖLLISCI AGEHL  LOOBROGELICTIGSSIGABITERTERVI VI ÜLEN ÜLESCI AGEHL  FERBLELLEBMIKWISSVIJOROTESTERKERNTÜDASHPERTYAGLI  TÜLT VARAHETYLLEKSRAVEONKOERTPELITYÖLLISCI AGEHL  FERBLELLEBMIKWISSVIJOROTESTERKERNTÜDASHPERTYAGLI  LANTEBELTEMIKWISSVIJOROTESTERKERNTÜDASHPERTYAGLI  LANTEBELTRILIVERLINGUEROVIÇAGINGTORDERVETVAGIL  LANTEBELTRILIVERLINGUEROVIÇAGINGTORDERVETVELU  DÜÇÜN CÜLLERRANFOVI ALLDERCOPP RATETVETVELUORO  GÜRKERGERFÖRÜNGULAPHET IHTERLÜGEST GÖRE I DEMORDING  KRÖMFETTÖÖLÜN FÜL TÜLERGE GÜRSE I DEMORDING  KRÖMFETTÖÖLÜN FÜL TÜLERGE GÜRSE I DEMORDING  KRÖMFETTÖÖLÜN FÜL TÜLERGÜRÜN TÄLDERÜN FÜR TÜN  NAI PROFRONKONAUSTER ILLEGEN FÜR TÜLEN FÜR TÜLERGÜNEN  KRÖMFETTÖÖLÜN KÜRELIKTAMI TERRÜNDIN VICH TÄNGENDEN  KRÖMFETTÖÖLÜN FÜL TEPAUN TÜLEN KÜREPARIKLÜNEN FÜL  LERBEDLIKT ITT IT FPAUN CONTAUT KABEGLAKUNERLINKUR  RALLERBENDIK I TÜLT IT FPAUN TÜN KÜRKKRÜNENLILLE  BEREDLIKT I TÜLT FPAUN TÜR KÜRKREBELLLEDENSELLIKVÜR  RALLERBENDIK BERKERBERIOOLLERVIT KABEGLAKUNERLINKUR  BRALLERBENDIK ELT DELLE KÜREBERLILLEDENSELLERUR ELBEGLORDER FÜR KENNERLINGENER FÜR  BERKERKRONGLER KÜRBERLICHER KÜRBERELLEDEN KENNERLINGENER FÜL  BERKERKONGLER KÜRBERLICHER KÜRBER FÜLLEGENSER  BERKERKONGLER KÜRBERLICHER KÜRBER FÜLLEGENSER  BERKERKONGLER KÜRBERLICHER KÜRBER FÜLLEGEN KENNERLINGEN FÜR  BERKERKONGLER KÜRBERCHLER KÜRBERGEN ELLEGEN KENNERLINGEN FÜR  BERKERKEN BERKERTERUNG LERGEN FÜL KREMBERLICHERDEN FÜL  BERKERKEN BERKERTEN BERKER BERKERTERGENDEN FÜLDEN KENNERLINGEN FÜR  BERKERKEN BERKERTEN BERKER BERKERTERGEN FÜR KÜRLERGEN BERKERTERGEN FÜR KENNERLINGEN FÜR  BERKERKEN B
5931	223	6082	MARKICLEROLERABERATEMANGERICORELDATEMEGISE  FORTINITALIBRODITS SESSISSISSICALIBROSILERADEDOTES  TSONIETO POGE  RECOPETI PEPTINAGE POLEDERE LE FYDRAVITHOATGAINTAK  ENCLIPET PETINAGE POLEDERE LE FYDRAVITHOATGAINTO DE LO  ENCLIPET PETINAGE POLEDERE PETINAGE POLEDERE  LOCREDOS IL CTICESCAGNITENTIKKY LOYLANYASSHKORKOHN  TOYI YOAN IETYLLEKSRAVEON KORFTEI TYOLLSS JACEHL  LOCREDOS IL CTICESCAGNITENTIKKY LOYLANYASSHKORKOHN  TOYI YOAN IETYLLEKSRAVEON KORFTEI TYOLLSS JACEHL  PSENELI LISHLEKVOS VOLGOTTIS PEKERNTÜDASKPERTYAGLI  LOCREDOS IL CTICESCAGNITENTIKKY LOYLANYASSHKORKOHN  TOYI YOAN IETYLLEKSRAVEON KORFTEI TYOLLSS JACEHL  PSENELI LISHLEKVOS VOLGOTTIS PEKERNTÜDASKPERTYAGLI  LOLLOGRÜNDET TALLI LICH EL VOLGOTTIS POLGOTTIS PERINGENTO  SERVICIONAL LICHARIS PERINGEN PERINGEN TÜR  SEROLLILORIN TALLI LICHARIS VOLGOTTIS PERINGEN TÜR  LOCREDOR PERINGEN PERINGEN PERINGEN PERINGEN TÜR  LOCREDOR PERINGEN PERINGEN PERINGEN TÜR  LORGINGEN PERINGEN PERINGEN PERINGEN TÜR  LORGINGEN PERINGEN PERINGEN PERINGEN TÜR  LORGINGEN PERINGEN PERINGEN PERINGEN PERINGEN TÜR  LORGINGEN PERINGEN PERINGEN PERINGEN PERINGEN TÜR  LORGINGEN PERINGEN PE
5931	113	6082	MARKICLERGUERABERATEANARGERICOREUDATEANEGUSE  EVETTLINGUERADOT ESTESSISSISSICIALHEGISLEELESDOTESI TSÖNNETÜPEÖGE  RÖNCHET VEPTIKAGE TÜLEDERE ELFVÜRAVITHERATGADITAK KÜMTI SERNIGFERASITERERGDEWWIELABIOKEAMINDOID  RÖNCHET VEPTIKAGE TÜLEDERE ELFVÜRAVITHERATGADITAK KÜMTI SERNIGFERASITERERGDEWWIELABIOKEAMINDOID  RÖNCHET VEPTIKAGE TÜLEDERE ELFVÜRAVITHERATGADITAK KÜMTI SERNIGFERASITERERGÜERWIELABIOKEAMINDOID  LOOBROGELICTIGSSIGABITERTERVI VI ÜLEN ÜLE BERGENETIT  TÜLT VARAHETYLLEKSRAVEONKOERTPELITYÖLLISCI AGEHL  LOOBROGELICTIGSSIGABITERTERVI VI ÜLEN ÜLESCI AGEHL  FERBLELLEBMIKWISSVIJOROTESTERKERNTÜDASHPERTYAGLI  TÜLT VARAHETYLLEKSRAVEONKOERTPELITYÖLLISCI AGEHL  FERBLELLEBMIKWISSVIJOROTESTERKERNTÜDASHPERTYAGLI  LANTEBELTEMIKWISSVIJOROTESTERKERNTÜDASHPERTYAGLI  LANTEBELTRILIVERLINGUEROVIÇAGINGTORDERVETVAGIL  LANTEBELTRILIVERLINGUEROVIÇAGINGTORDERVETVELU  DÜÇÜN CÜLLERRANFOVI ALLDERCOPP RATETVETVELUORO  GÜRKERGERFÖRÜNGULAPHET IHTERLÜGEST GÖRE I DEMORDING  KRÖMFETTÖÖLÜN FÜL TÜLERGE GÜRSE I DEMORDING  KRÖMFETTÖÖLÜN FÜL TÜLERGE GÜRSE I DEMORDING  KRÖMFETTÖÖLÜN FÜL TÜLERGÜRÜN TÄLDERÜN FÜR TÜN  NAI PROFRONKONAUSTER ILLEGEN FÜR TÜLEN FÜR TÜLERGÜNEN  KRÖMFETTÖÖLÜN KÜRELIKTAMI TERRÜNDIN VICH TÄNGENDEN  KRÖMFETTÖÖLÜN FÜL TEPAUN TÜLEN KÜREPARIKLÜNEN FÜL  LERBEDLIKT ITT IT FPAUN CONTAUT KABEGLAKUNERLINKUR  RALLERBENDIK I TÜLT IT FPAUN TÜN KÜRKKRÜNENLILLE  BEREDLIKT I TÜLT FPAUN TÜR KÜRKREBELLLEDENSELLIKVÜR  RALLERBENDIK BERKERBERIOOLLERVIT KABEGLAKUNERLINKUR  BRALLERBENDIK ELT DELLE KÜREBERLILLEDENSELLERUR ELBEGLORDER FÜR KENNERLINGENER FÜR  BERKERKRONGLER KÜRBERLICHER KÜRBERELLEDEN KENNERLINGENER FÜL  BERKERKONGLER KÜRBERLICHER KÜRBER FÜLLEGENSER  BERKERKONGLER KÜRBERLICHER KÜRBER FÜLLEGENSER  BERKERKONGLER KÜRBERLICHER KÜRBER FÜLLEGEN KENNERLINGEN FÜR  BERKERKONGLER KÜRBERCHLER KÜRBERGEN ELLEGEN KENNERLINGEN FÜR  BERKERKEN BERKERTERUNG LERGEN FÜL KREMBERLICHERDEN FÜL  BERKERKEN BERKERTEN BERKER BERKERTERGENDEN FÜLDEN KENNERLINGEN FÜR  BERKERKEN BERKERTEN BERKER BERKERTERGEN FÜR KÜRLERGEN BERKERTERGEN FÜR KENNERLINGEN FÜR  BERKERKEN B

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Jamino acid segment containing signal peptide Analamine, C-Cysteine, D-Aspartia Sidi, Re- Clutamic Acid, P-Phanylalamine, G-Clycine, H-Histidine, I-Isoleucine, K-Lysine, L-Leuckine, M-Methlonine, N-Apparagine, P-Proline, O-Cultamine, R-Aryinine, S-Serine, T-Threonine, V-Walline, M-Tyrybophan, Y-Tyrosine, X-Wunknown, *-Stop Codon, /-possible nucleotide deletion, V-possible nucleotide disertion)
	ogumo		F.KKLLKORBALSCRLEEKALATDKEFTERRY.QBLDDLTVDLD HOROVASHLEKKG, KETPOLLAEBISI SARTJESEDBARBARBE HOROVASHLEKKG, KETPOLLAEBISI SARTJESEDBARBARBE ETTALGELGADEBARBAKEBEEFERGÜNGLADEWENDISSCRÜNG HOROVASHLEKKG, KETPOLLAEBISI SARTJESEDBARBARBE ETTALGELGADEBARBAKEBEEFERGÜNGLADEWENDISSCRÜNG HOROWING HOROVASHLEKER BERNEHER BENEHER BERNEHER BENEHER B
5932	33	572	RHLEEICFLPLOKGRKLK.SGPRWEEGKPROTOGLWYKAEANWO FGATLAVGLTIFYLSVVTIIICFTCSCCCLYKTCRRPRPY\APP PEPP/SVVHAPPYGPSSVPSSYGPSYGVGHMPPGQOKPAPY PMOYPDFYROPMGPPAYHETLAGGAARFYPASQPPYNPAYMDA PKRAL PKRAL
5933	1	3190	OTHEL KYADATYPOSSOCANSITYRSINYESSISSISSISSIANDIASOPSIS DIPPETERPSICHIYYMISSIASISICLOSINGIALISELL
5934	1	3190	CHELLMAN, NERVISONAS STRESS DIVISES SSEDIJUSTOS SSEDIJUS SSEDIJA SSEDIJUS SSEDIJUS SSEDIJUS SSEDIJUS SSEDIJUS SSEDIJUS SSED

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
: CM	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
			QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE
	í	i	SKFSKYSEMSZEKRAKLREIELKVMKFQDELESGKRPKKPGCSF
		I	QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
			DECTPTREERKRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
			SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSRSP
			KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
	l .		LCPERSVF
5935	3	4493	SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL
	1		SDSGSFVSSRARREKKSKKGRQEALERLKKAKAGERYKYEVEDF
	i		SDSGSFVSSRARRBRRSKNGRQEADERDRAARAGERYRYEVEDF
	1	1	TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
			LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
	1	1	GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
i			IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
		1	DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
- 1		1	KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
		l	VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF
1		[	GKVWIESAETHVSCCVMVKNIERTLYFLPRENKIDLNTGKETGT
1			PISMKDVYBEFDEKIATKYKIMKFKSKPVEKNYAFEIPDVPEKS
1		Į.	EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK
			GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKEVSPPPLV
			VMAFSMKTMONAKNHONEIIAMAALVHHSFALDKAAPKPPFQSH
			FCVVSKPKDCIFPYAFKEVIEKKNVKVEVAATERTLLGFFLAKV
- 1			HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKRSNM
- 1			PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ
- 1			ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC
ı			ELNVLPLALQITNIAGNIMSRTLMGGRSERNEFLLLHAFYENNY
- 1			IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL
- 1			DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASEAQKV
1			TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
			LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT
1			YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEEVFKL
			GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD
.			GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
- 1			ENIQKELIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
i			HVHVALWINSQGGRKVKAGDTVSYVICODGSNLTASORAYAPEO
- 1			LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL
			\DFTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
			TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN
- 1			KLIMDIRRPIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
			ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK
			LKKQFFTPKVLQDYRKLKNTABQFLSRSGYSEVNLSKLFAGCAV
5936			KS
3936	1124	139	RGEEQFDA3FRR FACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
			RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS
- 1			NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL
- 1			PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI
	J		SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN
	ļ		SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD
- 1			SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
- 1			QEQASSGWGSRIRGDGSGFSL
5937	31	1600	PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL
			YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI
			LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK
			LVKNAQDKIELHLFMLNGLPDNVFRLTEMEVLSLELIPEVKLPS
			AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMCK
			IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
			IPRWVFHLKNLKELYLSGCVLPEQLSTMQLBGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS
			IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLOKLSLDNEGSKLVVLNNLKKMVNLKS LBLISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ
		·	IPRWVFHLKNLKELYLSGCVLPEQLSTMQLBGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS

SEO	Predicted		
ID	beginning	Predicted end	Aminc acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LFOCKKLOCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
-		1	PPELEGCQSLKRNCL_VEENLLNTLPLPVTERLOTCLDKC
5938	395	1865	YKGEGFFCNQBARGERRKKKKAMSSPNIWSTGSSVYSTPVFSOK
	1	1 2000	MTVWILLLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
		I	MIT VALIDADES I FOR I SQUESDED I EDIAS NEI WYLIPE V PEGDY
			TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
		i	YTIDIFFAQTWYERRLKFNSTIKVLRLNSNMVGKIMIPDTFFRN
			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDARCQLQLHNFP
	1	I	MDEHSCPLEFSSYGYPRESIVYQWKRSSVEVGDTRSWRLYQFSF
- 1	l		VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
- 1			VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
1		1	YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK
1			KNPAPTIDIRPRSATIOMNNATHLQERDEEYGYECLDGKDCASF
			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
1			VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
	1	1	LLKANVEKPVKMLIYSSKTLELRETSVTFSNLWGGGGLLGVSIR
1			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
1			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
		i	
			LGCGIGYCYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE
	i		VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
1	1	J.	PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
	1		PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSNPPRNLPG\I
			APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
			VDANASESP
5940	145	717	RRSASRSASPROSACTAVITGTRAGGTCLAAAHHRMRWRADGRS
			LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
			QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV
	1		LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT
	1	ļ.	PW/AAPAOWAAPITI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPPCCGGSLLAVVVLLALPVA
- 1	1		WGQCNAPEW\LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPF
1	1		SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGKVHVIKGIQFGSQ
	1		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
J	1		TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
	i		CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
	1		
J			NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
1			VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW
			SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
	i		QLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSPPVIPNGRHTG
			KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG
	1		VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
	1		CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
	1		VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI
			CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
		1	FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
		i	VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWSPELPS
1			CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAA
1		i	SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA
	1 1		KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
	i l		PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTT
	1		RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD
1	1		FPIGTSLKYBCRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
1		J	
1		J	PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
1	1		TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
1	1	1	CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
1			TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVXCQA
1	1		LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
	1		EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
1		1	LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSL/NNSVP
	i		VCBHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence	sedacuca	\=possible nucleotide insertion
	bequence		(=possible nucleotide insertion)
	ł	i	TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF
1			PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLENLVWS
			SVEDNCRRKSCGPPPEPFNGMVHINTDTCFGSTVNYSCNEGFRL
			IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN
1	I.		RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVW
			SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPG
1			FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ
1			DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKS
1			CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRSASHCV
	1		LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLCDIPYGKE
	1		VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPAPRCEL
1			PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDFGYLLVGK
1			GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY
1			GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRTHDALI
1	1		VGTLSGTIFFILLIIFLSWIILKERKGNNAHENPKEVAIHLHSQ
			GGSSVHPRTLQTNEENSRVLP
5942	4509	588	YLYVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRKL
1			DK\AQMIRFEERTGYFSSTDLGRTASHYYIKYNTIETFNELFDA
1			HKTEGDIFAIVSKAEEFDQIKVREEE:EELDTLLSNFCELSTPG
			GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA
			LFEIALRKRWPTMTYRLLNLSKAIDKRLWGWASPLROFSILPPH
			MLTRLEEKKLTVDKLKDMRKDEIGHILHHVNIGLKVKQCVHQ1P
			SVMMEAFIQPITRTVLRVTLSIYADFTWNDOVHGTVGEPWWIWV
1			EDPINDHIYHSEYFLALKKQVISKEAQLLVFTIPIFEPLPSOYY
1			IRAVSDRWLGAEAVCIINFQHLILPERHPPHTELLDLQPLPITA
			LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPTGSGKT
			VAAELAIFRVFNKYPTSKAVYIAPLKALVRERMDDWKVRIEEKL
1	l i		CHARLE LEGISLED MAGAIN TARREST AND AN AN AN AN AN AN AN AN AN AN AN AN AN
	'		GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQNRNYV QQVTILIIDEIHLLGEERGPVLEVIVSRTNFISSHTEKPVRIVG
			LOWAL AND DOLD MAN MAN OWN PARTY AND DAMES OF THE PARTY O
			LSTALANARDLADWLNIKQMGLFNFRPSVRPVPLEVHIQGFPGQ
			HYCPRNASMNKPAFOAIRSHSPAKPVLIFVSSRRQTRLTALELI
1 .			AFLATEEDPKQWLNMDEREMENIIATVRDSNLKLTLAFGIGMHH
1			AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNFPAHLVIIKG
			TEYYDGKTRRYVDFPITDVLQMMGRAGRPQFDDQGKAVILVHDI
			KKDFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSKQDALD
1 1			YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE
			LSYCIBIGEDNRSIEPLTYGRIASYYYLKHQTVKMFKDRLKPEC
1			STEELLSILSDAEEYTDLPVRHNEDHMNSELAKCLPIESNPHSF
			DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML
1			DVAANQGWLVTVLNITNLIQMVIQGRWLKDSSLLTLPNIENHHL
1			HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFSSMVES
			ELHAAKTKQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST
1 1			LTADKRODNKWIKLHADQEYVLQVSLQRVHFGFHKGKPESCAVT
1			PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHHVASLSFYT
1 1			PBIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ
H			GL
5943	1	2274	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR
1	1		EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD
1			GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL
1	1		LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP
1	1		VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR
	I		EPQTPTNVIILSEABEESLVLNKGRAYTASLGBTAVAFDFGPLA
1			AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I
1	1		WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML
	i		YHCVVLEGRREDDHTSEKSWDSRIDLIPSLYVFECVELELALKL
1 1			ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI
			HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP
j		1	IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR
			EDVEVAESPLRVLAETPDSFEKHIRSILORSVANPAFLKASEKD
	1		IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ
		İ	KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK
			,, ,

SEQ	Predicted	Predicted end	I have a second and a second an
ID			Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	D-Deeline, G-McChiloffine, Negaparagine,
1			P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amine acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	bequence		(=possible nucleotide insertion)
	1		KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
1	l		KDYQQQKMEKVLSLPKPTIILSAYQRKCIOSILKERGEHIREMV
1		i	KÇINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
1		] 3120	
1	l .		ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
1		1	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
1			KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
i			GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
			COLL COCCOUNTS TO DOMESTING TO A STATE OF THE STATE OF TH
	i		SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
			TROATOLINALIKOPOKEIDELIPKNRLKSSSANSKIGSSAPTT
			TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
	l .		VN\NVRPGFPVSFP\LAYPPPQFAHALLAAQTFQQIRPPRLPMT
1		i	HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNQNSS
1	I	l	GEOLING GEL MEG DE PER VELLE PARCAL INSPAPRINVERHSNONSS
1	I	I	GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
i	1		VTVVKTSNATTTTVTTTASNENTAPTNATYPMPTAKEHYPVSSP
1	I	I	SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEOEAGSPPVVET
1	I	I	TNTRPPNSSSSSSSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP
			EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
	1	l	
			PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ
			LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
			SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
i			FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGOM
			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
			CUDA FOR DOCUME COMMON OF THE
			GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG
i			TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
1			IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
			VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
			MVSSSTENNGPOTVWTGPWAPHMNSVHMNOLG
5945	1461	197	
3343	1401	197	GVTHLFLFGKRKLRNGTAEDLKGQADFFFLLVSEAVVATGSPRA
			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ
			QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
1			KRKKRRIMKAPAABAVAEGASGRHGQGRSLEAEDKMTHRILRAA
			QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
1			A NUCYL I CD CA AND CHOCK CORDS A OF A DD A CORD IN THE BUILDING
			AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
			GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP
			QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV
1			LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
			REBRRREE\KDRAWERDLRTYMNLEF
5946	541	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
1	571	4000	ADGGROUP AT A STANDARY TO A ST
1			SEGSPORVNSIDFV\EL\BHLQPDVLVHAVLRVVDF/TILTEAV
			YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
			YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
1 1			KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ
			KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKOCF
	J	Į.	SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
	ı	J	
1 1		J	DCLMRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
			DENSYPLOQDFSLLDFYPDIVKHGANARL
5947	3	1317	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEGGFGAPCLKCKEK
1 1			CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
1 1			
	I	1	KYTTLIAKLKSDGIPMYKRNVMILTMPVAAKKNVSINTVTYEWA
			PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD
			QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG
			PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG
i			DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG
ı I	1		DATE OF THE PROPERTY OF THE PR
ı I			RHYCDSEKPRCAGCDBLIFSNEYTQAENQNWHLKHFCCFDCDSI
		- 1	LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN
	1		NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
5948	39	3370	YRBRYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGP1DO
			GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
		1	ON TOPICAL OR CHROSEARCH PSSPCSV KHSPTKETLTYAQAQRM
	1		VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Scrine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	secuence	- and another	\=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSABELDNEVEYDMDEEDYAWLEIVNE
			KRKGDCVPAVSQSMFEPLMDRFEKESHCENQKQGEQQSLIDEDA
1			VCCICMDGBCQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
	_		E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
- (	1		QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
			YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1			KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
fi .	i		FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
			KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
1	ł		MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1			FYRAAVRIRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
1	l		RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
			SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEKSPGKRLDAGL
	i .		TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
1			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
			CQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
	1		PGHHNGVTIPAPPLDVLKIGEHMOTKSDEKLFLVLFFDNKRSWO
J	'		WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
			SRVHGEPTSDLSDID
5949	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
			GNHYOMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAOAORM
			VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
	i l		PVCLRTKRHKNNRVKKKNBALPSAHGTPASASALPEPKVRIVEY
			SPPSAPRRPPVYYKFIEKSABELDNEVEYDMDEEDYAWLEIVNE
			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
			VCCICNDGECQNSNVILFCDMCNLAVHQBCYGVPYIPEGQWLC/
1 .			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1 1	1		QCHKANCYTAFHVTCAQKAGLYMKMEPVK3LTGGGTTFSVRKTA
1			YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
			KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAICRKKQ
1			FVERAHSYNLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
1			KHPMDFATMRKRLBAGGYKNLHEFEEDFDLIIDNCMKYNARDTV
1 1			FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
1 1			RRPFSWEDVDRLLDPANRAHLGLESQLRELLDMLDLTCAMKSSG
1 1			SRSKRAKLLKKBIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
	1		TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
1 1			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
] [			GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
1 1		J	PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWO
1 1			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
			SRVHGEPTSDLSDID
5950	1166	373	BSRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
	1		CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPO
1			DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
] [		ļ	SSSGGSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
1			KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAOGR
			LTRVLLTASTLKSIPTSLLGDLFFRPIIGDVDIAGLLGDMLLLR
5951	143	5449	WAVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
1 1			VEQDSKETVKLSHEDDHILEDAGSSDISSEAACTNPNKTENSLV
1		-00-	GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIEPLGYCEDA
1		Y	ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDQNSK
1 1	1	1	QLNAIBSTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKD
		I	VIHSKONMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
			QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ

SEO	Predicted	Predicted end	Amino acid segment containing signal peptids
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first		L-Leucine, M-Methionine, N-Asparagine,
		amino acid	P=Proline, Q-Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSOK
		1	QCHKPQQQAPAMKTNSHVKBELEHPGVEHFKBEDKLKLKKPEKN
		i	LOPRORRSSKSFELDEPPLFIPDNIATIRREGSDHSSSFESKYM
			WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSOAQOM
1			GEEDKEYYCYKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
		l	CEKLGLSKHTTNERTKYIDDTVKHKVKILKRESGEGRNSSDCRD
		I	
			NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
1	!	ł	HSLKDILMKRLTDSNLKVPEBKAAKVATKIEKELFSFFRDTDAK
1	1		YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
	i		KELAAWRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
			APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
1	1		QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
1	1	1	AESIADALSSTSNILASEFFEEEKQESPKSTFSPAPRPEMPGTV
1	I	1	EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
1	I	1	PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
1			SYTLLFAYFSSRKRYGVAANKMKQVKDMYLIPLGATDKIPHPLV
			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHTAETPESA
			PPIALPPDKKSKIEVSTE3APEEENDFFNSFTTVLHKORNKPOO
			NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENOPTTLEL
1	f .		ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
1			
1	]		TNSKIEKTDNVEVTDGENKEIKVKVDN1SESTDKSABIETSVVG
1			SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
1			KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
1			LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
1			HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
1	l .		PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
1	l .		VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS
1			SPPGFPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\ONPM
1	1 :		VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPONFYQVKDIRRPE
			RRHSDFWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
			WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD
			GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
			KDRDHTDRTKSKR
5952	3226	639	
1 5552	3220	633	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
			ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
			QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
	1		QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
1			QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
] [			EQYESFEIIAFATTPDGYTPELPLPLIIKIEDENDNYPIFTEET
1			YTFTIFENCRVGTTVGQVCATDKDEPDTMHTRLKYSIIGQVPPS
i l			PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMDGQYFGL
1			QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
			DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
1			NYEBKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE
	ļ		GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSJIRYKKL
	ļ ļ		TDPTGWVTIDENTGS IKVFRSLDREAETIKNGIYNITVLASDQG
	l l		GRTCTGTLGIILQDVNDNSPFIPKKTVIICKFTMSSAEIVAVDP
1			DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYONDPPF
1 1			GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
1			
			GGVQLGKWAIIAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
1 1			LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG
1			IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
			RYTYSEWHSPTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKBGQTIK
1			LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
1		J	KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
1		J	VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADLEAVLADVSYLMAMBKSKATPAARASKRIVL
1			PEPSIRSVMQKYLABRNEITFDKIFNQKIGFLLFKDFCLNEINE
1 1		1	AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH

- 1	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /-possible nucleotide deletion,
1		sequence		\=possible nucleotide insertion)
- [				PFSKQAVEHVQSHLSKKQVISTLFQPYISEICESLRGDIFOKFM
- 1		1		ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK
				ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI
				VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSBKEMRFYA
				TEILGLEHMHNRFVVYRDLKPANILLDEHGHARIS\DLGLACD
- 1		ľ	1	FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADWFSLGCMLFKLL
- 1			ĺ	RGHSPFRCHKTKDKHEIDRWILTVNVELFDTFSPELKSLLEGLL
				QRDVSKRLGCHGGGSQEVKEHSFFKGVDKQHVYLQKYPPPLIPP
				RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW
				QQEVTETVYEAVNADTDKIEARKRAKNKÇLGHEEDYALGKDCIM
			J	HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ
				ILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNE
- !				TPKEAQRLLRRAPKFLNKPRSGTVBLPKPSLCHRNSNGL
ĺ	5955	1726	444	KREREFRLAVCPLRYPSAYESSPGTELRECGLCRSGQEFADCRR
			1	PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ
ĺ		[		VWKRCINIWRDVGLFGVLNEIANSEEEVFEWVKTASGWALALCR
				WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT
				NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS
				VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA
- 1				WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVINLLW
				SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD
				GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL
ŀ	5956			ROOYRHOMVRRGLGERLTPWSGTPVGRVWLCL
	5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA
J				TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
				IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT
				FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR
				SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL
				LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK
- 1		1		AYSDSQEDEWLSAAIDCSBYLPDQMVVEISRSFPEQPDRTDLVK
				ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT
- 1				QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHOKDVFKIPGTL\HKI
Į				
- 1		1		VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE
H	5957	1479	451	LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIBHFGD
- 1	3331	1 17/5	451	ELQVAVAMOTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK
				GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV
- 1				SLKDIKNSKCPRGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG
				PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE
- 1				LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD
- 1				TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS
- 1				KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL
ŀ	5958	1	3138	AAALGMLLNFPACOAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD
- 1		_	9230	ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSACCRQIPF
-				DTTNNRKIRVNGTKEPIEFKSNOWFG\ATVKA\HKGKSCGPVAP
-1				LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP
-1				EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA
- 1	ı			NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ
-1				ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV
-1				VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL
				FRDPOILTGTETFGRFGSAMAHLGDLNODGYNDIAIGVPFAGKD
ı				QRGKVLIYMGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD
- 1			J	SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDACLLLHPMIIN
- 1			ļ	LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVOLD
				SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD
		I	ļ	ETEPROKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE
-		I	ļ	QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGJENHLMLIINAR
1	- 1	1	j	NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT
				RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNASINFDLOIRSS
	- 1	1	J	NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE
_				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F≈Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T-Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	į.		EPHKEEBVGPLVEHIYELHNIGPSTISDTILSVGWPFSARDEFL
Į.	Į.	Į.	LYIFHIQTLGPLCCOPNPNINPQDIKPAASPEDTPELSAFLKNS
			TIPHLVRKRDVHVVBFHRQSFAKILNCTNIECLQISCAVGRLEG
			GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
			AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
5959			TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
1			NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
1	I		LLATGGDNPNSLAIYRLPTLEPVCVGDDGHKDNIFSIAWISDTM
1	1		AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
			DIPKEDINPONCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
1	1		NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
		1	EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
5960	2853	870	PPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
2960	4053	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
1	l	I	LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
			VLETCMKSCGKRPHDEVGKPRFLNELIKVVSPKYLGSRTSEKVK
1		i	NKILBLLYSWTVGLPBEVKIABAYQMLKKQG\IVKSDPKLPDDT TFPLPPPRPKNVIPEDEBKSKMLARLLKSSHPEDLRAANKLIKE
	ł		
			MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG SSEDL\MKEL\YQRCBRMRPTLFPTGRVDTEDND\EALAEILOA
1	ĺ	l .	NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
	i e		PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
			PSGPSLDGTGWNSFQSSDATEPPAPALACAPSMESRPPAOTSLP
		}	ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
			NKSSSCSSPSSSATSLLHTVSPEPPRPPCQPVPTELSLASITVP
1 1			LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
1			LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
1 1			ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
			WGSL
5961	198	3147	SGBPRPRPGNMATCIGEKIEDPKVGNLLGKGSPAGVYRAESIET
			GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
1 1			FEDSNYVYLVLBMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT
			GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
			KHYTLCGTPNYISPETATRSAHGLESDVWSLGCMFYTLLIGRPP
			FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHOLLRRNPADRL
			SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
			STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
			FYTOWGNOETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
			SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
! !			NFFKEETSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPOTE
1 1			TVCQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA
			WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIOOECVF
1			GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIROKT
			KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
			PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
			PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYNRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
n ora data			PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR
on story Admin			PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYNRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
mi dayaha			PNGG\RGFFLA\DRPPSPT\DNISR\TSF\DNLPEKYMRYDYA RRFVQUNRSKSPKITVFTRYAKCILMENSPSADFSVPFYDGVKI HKTEDFIQVIEKTGKSYTLKSBSEVNSLKEEIKMYMDHANEGHR ICLALESIISRERKKTRSAPFPFIIIGRKPGSTSSPKALSPPPS VDSNYFTRARSFRHWMISAASFTQAFILMSENUTTAGIGLTT
THE COLUMN ASSESSMENT OF THE COLUMN ASSESSMENT			PNGG\BGFFLA\DRPPSPT\DBLISR\YS\DNLPEXYRKYQYA SRFVGLVRSKSPK\ITYFTRYAKCILMENS PGADFEVWFYGGVKI HKTEDFIGVIEKTGSTYTLKSESEVWSLKEELTMYMDHANEGHE ICIALESIISHERRYKTRAPFFPIIIGKFGSTSSPKALSPPS VDSNYFTERASFPRHWWHISAASPTQAPILMSWNTWISGLGUTT TASGIDISSNSLKDCLPKSAGLLESVFYKYVGMATQ\LTSGAW
			PNGG\RGFFLA\DRPPSPT\DNISR\TSF\DNLPEKYMRYDYA RRFVQUNRSKSPKITVFTRYAKCILMENSPSADFSVPFYDGVKI HKTEDFIQVIEKTGKSYTLKSBSEVNSLKEEIKMYMDHANEGHR ICLALESIISRERKKTRSAPFPFIIIGRKPGSTSSPKALSPPPS VDSNYFTRARSFRHWMISAASFTQAFILMSENUTTAGIGLTT
5962	20	2447	PNOG MGFFLA\DRPPSPT\DMISR\YSF\DMLDFKYRKKYGYA SERVQLIMESKESKHITYPFRYANGCLIMENS PRADBFWYPTGWYH HKTEDFIGVIEKTGKSYTLKSESEVNSLKEEIKWYMCHANBGUR ICLALESIISERERKITRSAPFFPILIGRKPGSTSSPKALGPFPS VDSNYPTRADSFURNYMISAASFTGAPILINSSWYTTSGGGUT- TASGIDISSNSLKOCLPKSAQLLESYPYKNYGWATQ\LITSGAW WQFNDSGGUYWQGWSSISTYSPRING\YTT\GGGERRELPDYIKG
5962	20	2447	PINGS (REFPEAD) DEPPSTY DRIERY (YSF ) DILLIPECTATION CORRECTIONS OF THE PROPERTY OF THE PROPER
5962	20	2447	PROG NOFFEAN DEPPENT DRIERY TO PULLPEKTÄRKYOTA.  REPULDINGSISKITTYPETA NOELEMEN BEGODEPENTÄRKYOTA.  RETERDIOVERSISKITTYPETA NOELEMEN BEGODEPENTÄRKYOTA.  RETERDIOVERSISKITTYPETA NOELEMEN BEGODEPENTÄR SERVISKITÄRE PROVINCIAL SERVISKITÄR
5962	20	2447	PMOS MOFFEAN DEPPENT DWISERY TO PNULPEKTARKYOTAN SERVOLVENSISSEN TYPETYRA VALUEMEN BEADE PHYPTOWYLL HATROD FOUNDERS TYPETYRA VALUEMEN BEADE PHYRIA SERVING LIKE BE TOWNHOLANGUIR LICALASI ISRSKEN KITERAF PET LIGK REGYSTS PALLOG PROMOTOR THE GREEN THE SERVIL SERVING PROMOTOR TO SERVIL SERVING PROMOTOR TO SER
5962	20	2447	ENGS MAGFELA DEPPSETUDATISE Y SE YONLDEKLYNKYTOKA SERVOLUMISISSKY TYPETA MAGFELAN SE GAGEFYFTICHTE SE SERVOLUMISISSKY TYPETA MAGFELAN SE GAGEFYFTICHTE SE SERVOLUMISISSKY TYPETA MAGFELAN SE SERVOLUMISISSKY TYPETA MAGFELAN SE SERVOLUMISISSKY TO MAGFELAN SE SERVOLUMISISSKY TO MAGFELAN SE SERVOLUMISISSKY TO MAGFELAN THE MAGFELAN SE SERVOLUMISISSKY TO MAGFELAN SE SE SE SE SE SE SE SE SE SE SE SE SE
5962	20	2447	PMOS MOFFEAN DEPPSTY DWISERY YS PONLEPKYMKYCHAKYCHAKYCHAKYCHAKYCHAKYCHAKYCHAKYCHA
5962	20	2447	ENGS MOFFEAN DEPPSTY DRIERY AS PUBLIFECTIONS TO SERVOUNDESSENS TYPETRANGELINES PROGRESSIVE TYPETRANGELINES PROGRESSIVE TYPETRANGELINES PROGRESSIVE TYPETRANGELINES PROGRESSIVE TO SERVICE PROGRESSIVE TO SERVICE PROGRESSIVE TO SERVICE PROGRESSIVE TO SERVICE PROGRESSIVE TO SERVICE PROGRESSIVE PROGRESSIVE TO SERVICE PROGRESSIVE PROGRESSIVE PROGRESSIVE TO SERVICE TO SERVICE PROGRESSIVE TO SERVICE TO SERVICE PROGRESSIVE TO SERVICE PROGRESSIVE TO SERVICE TO SERVICE PROGRESSIVE TO SERVICE TO SERVICE PROGRESSIVE TO SERVICE SERVICE TO SERVICE TO SERVICE SERVICE SERVICE TO SERVICE SERVICE SERVICE TO SERVICE SERVICE SERVICE SERVICE TO SERVICE SERVI

г	SEO	Predicted	Predicted end	
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
- 1	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	IVO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		amino acid	sequence	Codon, /=possible nucleotide deletion,
Į		sequence	-	\=possible nucleotide insertion)
-				FLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLFTSLSVEDA
- 1			ł	AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
1		l .	I	QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
				DEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
- 1		l		TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
				KKPEISFMFQDEIEDFLRKHIQDAPEEFISELABYLIKPLNKTY
				LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
				MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
				AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA
- 1		ł	l	AEACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT
1			l	SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG
-			l	LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS
				SIKDLVLKSRKSSVTEE
Н	5963	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQOGKKGAPGMP\GLMGSN
		l	1	GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
1			1	GOFGYFGIFGANGONGDFGIQGFFGASGLKGEPGATGSPGEPGY
			٠,	MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG
				AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
				GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
				CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
1			Į.	GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPFGISKEG
				PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
				RKGPNY
Г	5964	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRPGGMEEACOVOTTK
				RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
				PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFOL
				FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR
Į				KKHLNYTEFTQFLQLEHARQAFALKDKSKSGMISGLDFSDI
1				MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
ł				THE LIGHT TOWN TO THE PROPERTY OF THE PROPERTY
1				ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
1				LADLYNASGRITLADIERIAPLAEGALPYNLAELQRQQSPGLGR
				PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG
1	- 1			SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI
				KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI
				VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
				FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV
				TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG
1				TAARVFRSSPQFG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK
1				SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
	- 1			VVQPKAAVAATQ
$\vdash$	5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLOKCFLSRG
1		-	2470	
1	1			CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP
1	1			SQNLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
1				EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAREQSFAELGL
1				GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
1	- 1	j		TGQREAARIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL
1	- 1	i		YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG
1	- 1	J		GLWWPQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
1	- 1			MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVOVSCLRIP
1	- 1			AVRTVLKIPQRVVHDLDKLPPREGFLESFKKGWKNAEMTRQLRE
1				REQRMRNQLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS
				SSKPKSKYPWHDTLG
Н	5966	102	1925	
			4765	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
1		l l		YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
1				GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
	i			SDEFRLEDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
		1		RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
1		1		FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
1		1		KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMOKE
1	- 1			DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1				CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEOLKVT
	1			QBPRAKKGRRNQSVEPKKEEPEPETEAVSSSOBIPTMPOPIEKV
			i	SVSTOTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
_				

_	000	T		
	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide _	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
	NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine.
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
- 1		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, O=Glutamine, R=Arginine
		amino acid	residue of	S=Scrine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.		amino acid	sequence	Codon, /=possible nucleotide deletion,
- 1		sequence		\=possible nucleotide insertion)
-				Vipage nucleotide insertion)
		ı		KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
				EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISCTKKKQWCYNC
-	5967	102	1000	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
-	3307	102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
		1		YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
				GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
- 1		Į.		SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
-		f	!	RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
		1	İ	FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
				KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
		1		DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
				CDELELHORFLREGREWKSKNEDRGEEEAESSISSTSNEQLKVT
				QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPIMPQPIEKV
				SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
			ļ.	VDDAYCOUND TERRESTOR TO TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TROUT TO THE TR
			l .	KDRMKSDHKRETERVVREALEKLRSEMBBEKRQAVNKAVANMQG
		l .		EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
-	5968	81	2000	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
- 1 '		**	1288	VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP
1		l		RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLACTSLSVLWVYL
		l		ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLQPVVWSQYPQPKL
				LEHRPTQLLTLTPWLAPIVSEGTFNPELLCHIYOPLNLTIGVTV
				FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAAVPGVDLGDHPL
				LSSIPIQGHSHWEETSMRRMETISOHTAKRAHREVDYLECLDUD
i				MVFRNPWGPETLGDLVAAIHPSYYAVPRQQFPYERRRVSTAFVA
				DSBGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR
		!		EESHLNRHFISNKPSKVLSPEVLWDDRKPQPPSLKLIRFSTLDK
1				DISCLES
	969	1126	503	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKORRIAANKCLC
1				TOURECTED OF THE PROPERTY OF T
				TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI
				FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR
				GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP
<u></u>	970	316		GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
1 -	15 10	316	4712	SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG
				RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
1				KALEDLRANFYCELCDKQYQKHQBFDNHINSYDHAHKQRLKDLK
				QREFARNVSSRSRKDEKKQEKALRRLHELAEORKOARCAPGSGD
1		1		MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG
1				GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF
1		i		SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV
	J			GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE
1	i			PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES
1				KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS
1		1		KARAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA
1	J	ı		CVEROPORAL CONTROL OF THE CONTROL OF
	- 1	1		GKESQEGPKHPTGPFPPVLSKDESTALQWPSELLIFTKAEPSIS
	- 1	i		YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE
				PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE
	- 1	1		TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRKHKADTEEK
l l				SSKABSGEKSKKRKKRKRKKNKSSAPADSBRGPKPEPPGSGSPA
1	- 1			PPRRRRACDDSQRRSLPAEEGSSGKKDEGGGGSSSQDHGGRKH
				KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHO
1	- 1			KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRRSYSSSS
-				DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS
1	- 1	J	,	SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRSRSRS
1	- 1		J	SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR
ı	- 1			KNEWCHPCDPFPUCCDDDDTDGVTVDCCCDDDVTDGVTVDCCCDDVTDGVTVDCCCDDVTDGVTVDCCCDDVTDGVTVDCCCDDVTDGVTVDCCCDDVTDGVTVDCCCDDVTDGVTVDCCCDDVTVDCCCDDVTDGVTVDCCCDDVTCCCDCDVTCCCDDVTCCCCDDVTCCCCDDVTCCCDDVTCCCDDVTCCCCDDVTCCCDDVTCCCDDVTCCCDDVTCCCDDVTCCCDDVTCCCDDVTCCCDDVTCCCCDDV
1	- 1		ļ	KRSWGHESPEERHSGRRDFIRSKTYRSQSPHYFRSGRGEGPGKK
	- 1		J	DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL
	- 1	1		EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS
				LGNKPVLPLIGKLPATRKPNKKCBESGLERGEBQEQSETBEGPP
	. !	1		GSSDALFGHOFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG
		1		PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSOPGPVESSL
				LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1 .	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	F-Fiorine, Cadidiamine, Rarginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	Dequence		\=possible nucleotide insertion)
1	1	i.	TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFPASAALAPATPAL
			QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPHPHPQ
			PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
			SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
2000			FSGQDLQHPPSHGT
5971	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
			PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRN
ŀ			RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTRISTD
1			FDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPL
1		Į.	SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENP
			PFYGVIRWIGQPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY
			FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWEAY
1			LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF
1			CLFAFSSVLDTVLLRPKEKNDVBYYSETQELLRTEIVNPLRIYG
1	ľ		YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRV
			EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFIN
			SNLKFARAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT
1			PROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTOVHLHP
J		ļ	KRLNHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHY
	!	1	VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL
			KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5972	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVIRGCTFSTAVVSPSAMTO
			EPFREBLAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF
ł	ł		SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAENDYLRCAAGSCI
			PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWFGCKLVL
1			NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKKGSMS
1			DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVDDSV
			SGPHLSVTFFWILVACFPSAIASHVAABCPNKCLVEVLIAISSL
1			TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLLV
1	i .		LLLON (CDOUGUBURURURA LOCOCYA A GATT GURDRON
i	l .		LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG
			GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH ND
5973	65	. 2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHACMAEDEPDAKSPKTG
10,0	""	. 2007	MGDGKDDFGHIWAWKSNGIISNFKKSPHAGMAEDEPDAKSPKTG
1			GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
			NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
			HTDTCLPKQSVYDAYRKYCBSLACCRPLSTANFGKIIREIFPDI
1 1	1 1		KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
	l		EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
			LISARSAHAHVLKAMGLABEDEHAPRERSSKPKNGLENPEGGAH
			KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLQV
) )			NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP
			LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTQPR
1 1		i	GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAAKQD
1 1			IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
1 1			PWETWGSGGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGTVSK
1 1		Į.	GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
5974	4293	0000	DTAPOGNKDLKEHVLQSSLSQEHKDPKATPP
1 22/4	4473	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
1 1			LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
j J	J	j	TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1			DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
	1		EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
1 1	1	İ	VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
1 1			BNQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
1 1			QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
1			LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
	1		REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1			KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
j		i	ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
į į	[	1	MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHPPNQI\DD
$\perp$			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

SSQ Predicted Predicted and Amino acid segment containing to beginning uncleotide NO: nucleotide location corresponding to first to first amino acid amino acid amino acid segment containing to first to first amino acid amino acid residue of amino acid amino acid segment with the first to first amino acid amino acid segment with the first to fi	partic Acid, E- ne, G-Glycine, 'Elysine, sparagine, 'gginine, 'ine, 'Unknown, *=Stop 'deletion, ion) TIERUYDVDUSYATOLE 'OASKOINPKRPRAL
NO: mucleotide Ocation Corresponding to first amino acid amino acid emino aci	ine, G=Glycine, G=Lysine, Separagine, Gginine, Gine, Line, Winknown, *=Stop deletion, Line, GASKOINPKEPRAL GASKOINPKEPRAL
location corresponding corresponding to first to first amino acid amino acid residue of amino acid	<pre>(=Lysine, sparagine, rginine, .ine, .Unknown, *=Stop deletion, ion) (Step</pre>
corresponding to first to first amino acid amino acid residue of residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid	asparagine, ginine, ine, ine, iunknown, *=Stop deletion, ion) THEEVDYDVDSYATQLE QASKQINPKRPRAL
to first amino acid residue of sesidue of amino acid residue of amino acid amino acid sequence Coden, /=possible nucleotide	ginine, .ine, .Unknown, *=Stop .deletion, .ion) !TEEVDYDVDSYATQLE !QASKQINPKEPRAL
amino acid residue of S=Serine, T=Threorine, V=Val residue of amino acid W=Tryptophan, Y=Tyrosine, X- amino acid sequence Codon, /=possible nucleotide	ine, Unknown, *=Stop deletion, ion) TEESVDYDVDSYATQLE QASKQINPKRPRAL
residue of amino acid W=Tryptophan, Y=Tyrosine, X=amino acid sequence Codon, /=possible nucleotide	Unknown, *=Stop deletion, ion) TEEVDYDVDSYATQLE QASKQINPKRPRAL
amino acid sequence Codon, /=possible nucleotide	deletion, ion) TEEVDYDVDSYATQLE QASKQINPKRPRAL
	ion) TEEVDYDVDSYATQLE QASKQINPKRPRAL
	QASKQINPKRPRAL
EEQVVEDHRAVFQESIRWLEDEKALLEM	QASKQINPKRPRAL
AILBQKIDILTBLRDKVKSFRAALQBEE	DESTENCE PROPRET
BODGMIISGKINGAVISEMEDNESV	ANATHORITAGE (ETD
LESIFSLWP\DL\VPDGEIEPSP\ETPP	PPASSAKVNKIVKNRR
TV\ASIKNDPPS\RDNRVVGSARARPSQ	FPEQFSSAQQNGSV\S
DISPVQAAKKEFGPPSRRKSNCVKEVEK EKRAQDVDATNPNYEIMCMIRDFRGSLD	
VCVRKRPLNKKBTQMKDLDVITIPSKDV	
ENQTFRFDYAFDDSAPMEMVYRFTARPL	AMAUREN OF ADDITION
QTGSGKTHTMGGDFSGKNQDCSKGIYAL	ARROUFIMIER DNAKE
LELQVYATFFEIYSGKVFDLLNRKTKLR	VLEDGKOOVOVVGLOR
REVKCVEDVLKLIDIGNSCRTSGQTSAN	AHSSRSHAVFOIILRR
KGKLHGKFSLIDLAGNERGADTSSADRQ	TRLEGAEINKSLLALK
ECIRALGRNKPHTPFRASKLTQVLRDSF	IGENSRTCMIATISPG
MASCENTLNTLRYANRVKELTVDPTAAG	DVRPIMHHPPNQI\DD
LETQWGVGSSPQRDDLKLLCEQNEEEVS	PQLFTFHEAVSQMVEM
EBQVVEDHRAVFÇES TRWLEDEKALLEM AILEQKIDILTELRDKVKSFRAALQEES	TERADEDADS ANTOFE
5976 20 2949 VHHLHLTRVSVVVNLDIILRIAQQMSIK	DING THE UNITED THE
PEVSUMEVKDPNMKGAMLTNTGKYAIPT	IDMANDO (PKKM/DEF
FLPEEPSSSSEEDDPIPDELLCLICKDI	
BC_RTALLESDEHTCPTCHQNDVSPDAL	IANKFLROAVNNFKNE
TGYTKRLRKQLPSPPPPIPPRPLIQRN	LQPLMRSPISRQQDPL
MIPVTSSSTHPAPSISSLTSNQSSLAPP	VSGNPSSAPAPVPDIT
ATVSISVESEKSDGPFRDSDNKILPAAR	LASEHSKGTSSIAITA
LMEEKGYQVPVLGTPSLLGQSLLHGQLII	PTTGPVRINTARPGGG
RPGWEHSNKLGYLVSPPQQIRRGERSCY	RSINRGRHHSERSQRT
QGPSLPATPVFVPVPPPPPTTLPI GQP\PPAGYSVPPPGFPPAPANLSTPWVS	LPPGVPPPQFSPQFPP
APPLSREEFYREQRRLKEEEKKKSKLDE	SSGVQIARSNT_PITQ
KERRSFSRSKSPYSGSSYSRSSYTYSKS	SPACATRACEDIATION
RSHSRSYSRSPPYPRRGRGKSRNYRSRSF	RSHGYHRSRSRSPPYP
RYHSRSRSPQAFRGQSPNKRNVPQGETER	REYFNRYREVPPPYDM
KAYYGRSVDPRDPFEKERYREWERKYREW	WYEKYYKGYAAGAOPR
PSANRENFSPERFLPLNIRNSPFTRGRRI	EDYVGGQSHRSRNIGS
NYPEKLSARDGHNQKENTKSKEKESENAI	PGDGKGNKHKKHRKRR
KGEESEGFLNPELLETSRKSREPTGVEEN	
PVRDEPMDAESITFKSVSEKDKRERDKP	
SKKENIVKPAKGPQEKVDG\DVRDLLDLN TILNHHLPLRRMKKSL\EPP\EKLTLNQG	
BGLFORCOIRKANN	AK (TPKNKTSQKGKSE
5977 1363 1336 FLEDRGQVLSFPQCLSLHSINHILHPGAG	WAAGPATGW/PEVI.T
PVLKESKFKETGVITPEEFVAAGDHLVHI	CPTWOWATGRELKYK
AYLPTGKQFLVTKNVPCYKRCKQMEYSDE	ELEAIIEEDDGDGGWV
DTYHNTGITGITEAVKEITLENKENIRLG	DCSALCEEEEDEDEG
BAADMEEYEESGLLETDEATLDTRKIVE	CKAKTDAGGEDAILQ
TRTYDLYITYDKYYQTPRLWLFGYDEQRC	
VKKTVTIBNHPHLPPPPMCSVHPCRHAEV	
5978 160 3213 RDGARRWGGCCSPI/WARGFYRRFDLATS	
	GRRLRGQTAEPAGRQ
RPRREPBAMDEQSVESIAEVFRCFICMEK FSCIRRWLTEQRAQCPHCRAPLQLRELVN	LIKLARLCPHCSKLCC
LCSLTKHEENEKDKCENHHEKLSVFCWTC	CKWAEEVTQQLDTLQ
GGHTKPLAEIYEQHVTKVNEEVAKLRRR	LANCE CHUCALWOOMH
EAVRNAKDERVREIRNAVEMMIARLDTQL	KNKUTTIMGOKTSI-T
QETELLESLLQEVEHQLRSCSKSELISKS	
ASPVTTPVPPDFTSELVPSYDSATFVLEN	
LQVSGLCWRLKVYPDGNGVVRGYYLSVFL	
VEMVHQSCNDPTKNIIREFASDFEVGECW	GYNRFFRLDLLANEG
YLNPQNDTVILRFQVRSPTFFQKSRDCHW	
INNLKERLTIKLSRTQKSRDLSPPDNHLS	PONDDALETRAKKSA

SEO	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	mailypeophan, improving, kabikhowi, mageop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	seçuence		\=possible nucleotide insertion)
1			CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHEELSDGDL
1			DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDESTMSGENDV
1	j.	J.	EYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
1	l .		ATSSLEDIDPLILITHLEDLKERSSIENLWGLOPRPPASLLOPTA
1	i	1	SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMABVRCMKTDVKN
1			TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLODLGME
1			
			LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
1			NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDTLPKTE
			DRQCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL
	Į.		QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
1	1		QEEHTSVGGFHDSFMVMTQPPDEDTHSSFFDGEQIGPEDLSFNT
1	1-		DENSGR
5979	212	3665	
3575	1	3003	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
1	1		TTTLS?SGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK
Į.			LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
i			PDKTLILEVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
1			DTQNITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK
1	l		FTNASKIIKTDFGSPGEPQIIFCRSEAAHOGVITWNPPORSFHN
	[		FTLCYIKETEKDCLNLDKNLIKYDLONLKPYTKYVLSLHAYITA
	1		KVQRNGSAAMCHFTTKSAPPSOVWNMTVSMTSDNSMHVKCRPPR
	l I		
			DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK
1			AYFHNGDYPGEPFILHHSTSYNSKALIAFLAFLIIVTSIALLVV
			LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET
i			YKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNQNKNRYVD
1			ILPYDYNRVELSEINGDAGSNYINASYIDSFKEPRKYIAAQGPR
1			DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
			RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ
			FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
			TGTYIGIDAMLEGLEAENEVDVYGYVVKLRRCRCLMVOVEAOYI
			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
			FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVFLKHE
	1		LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI
	1		AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
			EGKQTYGDI EVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
			YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL
			LIHCRDGSQOTGIFCALLNLLESAETBEVVDIFOVVKALRKARP
			GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
1 1			WHICH ACTION OF DEATH AND ACTION OF THE PROPERTY OF THE PROPER
1			KVKQDANCVNPLGAPEKLPEAKEQAEGSE?TSGTEGPEHSVNGP
5980			ASPALNOGS
2280	3	2363	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
1 1			PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR
			PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP
			VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
, 1			CGAPGODTKAGSMLVEQSEKLRHLSTFSHQVLOTRLVDAAKALN
			LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN
1			TANKKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
[			VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL
1 1			ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR
			MINISTROTTON TON THE PROPERTY OF THE STATE O
			MLWEQIKQIIQRITWVSPPAITLEWKRKVAQBAIESLSASKLAK
			SICSOFRTRLMSSHEAFAASLROLEAGHSGRLEKTEDLWLRVRK
1			DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
			WGGHFFCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
1 1			SVIDYNYGGGSSIAVL:IMERLHRDLYTGLKAGLTLETRLOIAL
1 1			DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
j 1			MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
1			LPBAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG
	1		
5981		0510	DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST
2281	1	2519	GRRHSAAMKRPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL
1 1			DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
1			G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV
			ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIR

SEO Pres	licted	Predicted end	
	inning	nucleotide	Amino acid segment containing signal peptide
	leotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	tion	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
con	esponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	irst	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	no acid	residue of	S=Serine, T=Threonine, V=Valine,
res	due of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
amin	no acid	sequence	Codon, /wpossible nucleotide deletion,
sem	ence		\=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGRIFRSSDFAKNFVOTD
			LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
			VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
	1		CHARACTER CONTROL CONT
			GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
			SVGQEQFYSILAANDDMV#MHVDEPGDTGFGTIFTSDDRGIVYS
	l l		KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
			DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
1 1			MAPLSEPNAVJIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
			EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
1			RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
1 1	1		LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC
			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
			GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
i I			CTSNFLSPEKONSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
1			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
	- 1		DEDILE
5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
			GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMOIPR
1 1	1		POVERTI CUR CUCCOMOT INTERIOR DIVERS TO A MEDITICIONAL PR
			FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
1 1			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFQNDR
			SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
1 1			LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF
1			TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
1 1			EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
			AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEE
1	1		VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNFRFEAPLF
1	1		NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
			SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAOKIRM
1 1			TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
	Į.		EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
1 1	1		QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA
			VEEPSIC VEEPSIC
5983	248	1763	
3,03	240	1/03	EARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
			RQ\YSAATALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ
			DCKRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
	i		GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
1 1	- 1		DALSKYSECLKINNKECAIYTNRALCYLKLCCFEEAKQDCDQAL
			QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK
	- 1	j	MELEEVTRLLNLKDKTAPFNK3KERRKIEIOEVNEGKEEPGRPA
1	- 1	Į.	GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGOIINAL
i I		J	STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN
1 1	1	j	LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL
1 1		ļ	SDTPNNHFTLEDIQALKRQYEL
5984	755	1193	SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL
1 1			TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
1 1	1		
1 1			SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY
	i		
5985		1400	FHHSLRSISRFSSG
5985	22	1408	FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
5985	22	1408	FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
5985	22	1408	FHHSLRSISFFSSG RRVARRGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRVNSFSSBAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPBBPGFDRVADAK
5985	22	1408	FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
5985	22	1408	FHHSI.RSISRFSSG  RYMAPOTAEPAKARITVERGPÄREDLIGABERKAGVSERGDSGE RRPNDSIPSAAAMSHIQI PPGIJTEILLGGTTVEVLRGQPPDLWE FAVEYFIR.RAMPARGLGIGPPBGSGTBVADAX GOSGSBEDBDLEYPVSSERNERVSVCAETYNDEEBEDTDERVI HPKTDEGREGLOBACKDILLERVLDGGGISGWLDAMFERIIVKAD
5985	22	1408	FHHSI.RSISRFSSG  RYMAPOTAEPAKARITVERGPÄREDLIGABERKAGVSERGDSGE RRPNDSIPSAAAMSHIQI PPGIJTEILLGGTTVEVLRGQPPDLWE FAVEYFIR.RAMPARGLGIGPPBGSGTBVADAX GOSGSBEDBDLEYPVSSERNERVSVCAETYNDEEBEDTDERVI HPKTDEGREGLOBACKDILLERVLDGGGISGWLDAMFERIIVKAD
5985	22	1408	FHISLASISARSG  REVAROTATEARARE TÜREGRARBULAGAREKAGUSERGIDGÜG  RERNES IPSAAAGMSHIQ I PPOLITELLQGYTVEVLRQQPPDLYE  FAVEYTEL REARRAFASILFAATPEQGLEHPPESOCDRYADAK GOSSERBBEJÜREVEYPESRERKEVSCETTYPPOEREBÜTDRYAT  HEKTÜRGROKLÖBACKULLEKKLOGGUSGVILDEM FERTVEAD  BIVTJOGODIORIEVYTI SERTÜTÜL LYTEKMOTTENSOYÜNNESSE GE  BIVTJOGODIORIEVYTI SERTÜTÜL LYTEKMOTTENSOYÜNNESSE G
5985	22	1408	FIRISLASISENSIS  ERVARPOTABEARARTVERGRAREDLAGASERAGVSERGIDGG RENRIGSI DENAROMENICI JE POLITELLOGATYEVILAGOPEDLUS  REVERSI DENAROMENICI JE POLITELLOGATYEVILAGOPEDLUS  FAVETFER LERBARAPASUPLAPATYEDGICHEP PERSOPERVADAK GOSISSIRBREDIL MEY PURSOR SURREVSYCAET YN POEBBEEDTID PEVI  HENT DIGORCALORACICI LICHENICOGGI (SOVULDAP PERI VEAD  ERVI ZOGODODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT PES UVO YNNISSE PE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT ZOGODORNE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT ZOGODORNE  ERIN ZI ZOGODORNEY VI RROTTO IL LYTENNOT ZOGODORNE  ERIN ZI ZOGODORNE ZOGODORNE ZOGODORNE  ERIN ZI ZOGODORNE ZOGODORNE  ERIN ZI ZOGODORNE ZOGODORNE  ERIN ZI ZOGODORNE ZOGODORNE  ERIN ZI ZOGOD
5985	22	1408	PHHSLASISFSSO  EVARPOTABEARRYVERGREARDLAGASKROUSERGDSGR REPHRST BEARARRYVERGREARDLAGASKROUSERGDSGR REPHRST BEARARRYVERGREARDLAGASKROUSERGDSGR REPHRST BEARARRASVERGREARDCAGE TREPHRST BEARARRY GOSGISFREGELING PPESS FRORKTSVICHT TREPESSEDTURFAV GOSGISFREGELING PPESS FRORKTSVICHT TREPESSEDTURFAV BEARARRYVERGREARDCAGE REPHRST BEARARRYVERGREARDCAGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSCHRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRST REAL REAL REAL REAL REAL REAL REAL REAL
5985	22	1408	FIRISLASISENSIS  ERVARPOTABEARARTVERGRAREDLAGASERAGVSERGIDGGE REPRISTI PSÄNAROMENICIJ PSGLITELLOGTTVEVLEGOPEDLVE REVERSTER SERARARSVEJARATVEGLEGLERSPERSOFRRVADAK GOSESBERBEIL BEVERSOFRRVSVCAET TYRDEEEEDTDEVI REVETSTER SERGERSOFRRVSVCAET TYRDEEEEDTDEVI REVETSTER SERGERSOFRRVSVCAET TYRDEEEEDTDEVI REVETSTORGENSOFRRVSVCAET TYRDEEEEDTDEVI REVETSTORGENSOFRRVSVCAET TYRDEEEEDTDEVI REVETSTORGENSOFRRVSVCAET TYRDEEEEDTDEVI REVETSTORGENSOFRRVSVCAET TYRDEEEETDTEVI REVETSTORGENSOFRRVSVCAET TYRDEEEETDTEVI REVETSTORGENSOFRRVSVCAET TYRDEEEETDTEVI REVETSTORGENSOFRRVSVCAET REVETSTORG
5985	22	1408	PHHSLASISFSSO  EVARPOTABEARRYVERGREARDLAGASKROUSERGDSGR REPHRST BEARARRYVERGREARDLAGASKROUSERGDSGR REPHRST BEARARRYVERGREARDLAGASKROUSERGDSGR REPHRST BEARARRASVERGREARDCAGE TREPHRST BEARARRY GOSGISFREGELING PPESS FRORKTSVICHT TREPESSEDTURFAV GOSGISFREGELING PPESS FRORKTSVICHT TREPESSEDTURFAV BEARARRYVERGREARDCAGE REPHRST BEARARRYVERGREARDCAGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSCHRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRSLAGLENGTRET LYKNINGSEGE REAL MANT PRAATTVATSGRST REAL REAL REAL REAL REAL REAL REAL REAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Giutamic Acid, P=Phenylalanine, G=Glycine.
I	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid sequence	sequence	Codon, /=possible nucleotide deletion,
5986	1806	484	\=possible nucleotide insertion)
3366	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
			SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
1			GLRWTPKSPLDPDSGLLSCTLPNGF3GQSGPEGERSLAPPDASI
			LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
			EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
		i	SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
	1		QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
1	1	1	VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
1			RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
			DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL TV
5987	1806	484	
1 5507	1000	404	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
1	l		SPCCRFDSPRGPPPPRIGLICALMAEDGVRGSPPVPSGPPMEED
1			GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
1			LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
			EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG QNWLNDQVMMMYGDLVMDTVPEK\VHPFNSFFY\DKLRTKGYDG
1			VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
			RTLMRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
1 .			DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
1			TO TO THE PROPERTY OF THE PROP
5988	1292	410	PKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ
			RLDCIYLNAGIMPNPQLNIKALLFGLFS\AEGLLTQGDKITADG
! !			LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
			FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
1			PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTE
			ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE
			KFYQKLLELEXHIRVTIQKTDNQARLSGSCL
5989	194	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA
1 1		'	ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFNYTAKLSLSPE
			NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNAEALAT
i I			EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
1 1			SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALSESS
1 1			EQEMEVEPARKGEEEQKEQEEQEEEGAGPAEVKEEGSOLENGEA
1. 1			PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVTH
1 1			KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK
1			AHEKTHSPLKPYGCEECGKSYRLISLINLRKKRHSGEARYRCED
1			CGKLFTTSGNLKRHOLVHSGEKPYOCDYCGRSFSDPTSKMRHLE
1			THOTOKEHKCPHCDKKFNOVGNLKAHLKIHIADGPLKCRRCGKO
			FTTSGNLKRHLRIHSGEKPYVCIHCOROFADPGALORHURTHTG
1 . 1	- 1	į.	EKPCQCVMCGKAFTQASSLIAHVROHTGEKPYVCERCGKRFVOS
'	. 1	ļ	SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY
1		ļ	LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
1	1	J	VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
1	I	ļ	VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
	I		FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE
F-200			TSPTAPECPPPAE
5990	2	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
1			SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS
	i		LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
1 1			PRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDFP
1 1			MHLACPEBEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN
, ,			LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV
1 1	J	,	VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL
1 [		- 1	CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP
1 1	l	J	GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS
		1	QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN
( I	1	1	LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS
		!	PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA
			EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *+Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			DPVPNDLTPVDPVLVKSRPTDPRRGAVSSALGGSAPQLLVESES
			LDPPKTIIPEVKEVVDSLKIESGTSATTHEARPRPLSLSEYRRR ROORQAETEEKSPOPPTGKWPSLPETPTGLADIPCLVIPPAPAK
1			KTALORSPETPLEICLVPVGPSPASPSPEPPVSKPVASSPTEOV
			PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS
i			LPPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP
			CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY
			GPLGWGPGPQHAPFWSTVPPPPLPPASIGRAVPQPKMESRGTPA
			GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKPVPASPHPK HKVSALVQSPQMKALACVSABGVTVEEPASERLKPETOETRPRE
1			KPPLPATKAVPTPRQSTVPKLPAVHPARLRKLSFLPTPRTQGSE
1			DVVQAFISEIGIEASDLSSLLEQFEKSEAKKECPPPAPADSLAV
			GNSGGVDIPQEKRPLDRLQAPELANVAGLTPPATPPHQLWKPLA
1			AVSLLAKAKSPKSTAQBGTLKPEGVTEAKHPAAVRLQEGVHGPS
1			RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRWNVKRHQDI
ľ	l .		TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS SLLSPEASPCRNDMNTRTPPEPSAKORSMRCYRKACRSASPSSO
1	1		GWQGRRGRNSRSVSSGSNRTSEASSSSSSSSSSSRSRSRSLSPP
			HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSSSSRSRSRS
			PSPRRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK
			IPGRMTRSELKQRFSVFGEISECTIHFRVQGDNYGFVTYRYAEE
	!		AFAATESGHKLRQADEQPFDLCFGGRRQFCKRSYSDLDSNREDF
5991	334	1379	DPAPVKSKFDSLDFDTLLKQAQKNLRR RLSSHFSOCSPSIYC\TKFDKOGNVTSFERKKTELYCELGLOAR
2337	334	1379	DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNLNLK
1			QWLFRELPSQLSGBGQLVTYPLPFEFRAIEALLQYWINTLOGKL
İ	İ		SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI
			KIFKESILRILDEBELLEELCVSKWSDPQVFEKSSAGIDHAEEM
1	ĺ		ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM
			RINLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL
5992	2	609	AGPDFRLVCGVSGSGFPGGROGOATEWRPLRPWNGAMEKLRRVL
3332	_	003	SGODDEECGLTAODSOINL/SEVLDASSLSFNTRLKWFAICFVC
1	l		GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK
	Į.		QLKKMFBATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
			FLSMTWYSLSYIPYARDAVIKCCSSLLS
5993	1650	594	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFCKVEKIGEGTYGVVYKAKNRETGGLVALKKIRLDLEM
			EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSO
1			DLKKYMDSTPGSELPLHLIKSYLFOLLOGVSFCHSHRVIHRDLK
1	1		PONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI
1	1		LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI
			FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG
			RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH
5994		1934	AGBVOLHVWIRGMRIOPO/KAAAIIDLDPDF8POSRPRSCTWPL
1	394		
	394	1334	PRPEIANOPSKPPEVEPDLGEKVHTEGRSEPILLDSRLDEPAGG
	394	1934	PRPEIANOFSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRLT
	394	1934	POPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIBSAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
	394	1934	POPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSXLLEGRSKA
	394		POPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRLT LAQIYEMWRTYPYRKDKGDSNSSAGWKNSIRHNISLHSKFIKV HNEATGKSSWMLNPEGGKSGKAPRRAASMOSSSKLLLGGRSKA PKKKPSGLPAPPEGHTTSPVGHFAKWSGSPCSRNREEADMWTT
	394		POPOLIGAVTOPRIGGSRRNAMONG YAGLISOAISSADERRILT LAQIYENWAYTEYPENGEDONSAGARINSIERHISLHSKEIKV INBATGKSSUMMLNPEGGESGKAPRRRAASMOSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPUGHFAKWSGSPCSRIKEEDDWHTT FRERSSNASVSTRISPIRESEVLAEEIPASVSSYAGOVPT
	394		POPOTLGAVTOPRKOGSRRINAKONOS YABLISQATESADERKIF. LAQITYEMWATVFYFEKKORDENSAGWINSITERHIISLHEKFIKV HINRATIKSSHHILIPBEGGISGKAPRERPAGENGSS KLLIGGRSKA PKKKPSGLFAPPEGATTEFYGHFARWISGFSCRINEREDAMET FREPRSSNASSVSTRILGPIREBESGLFARWITEFTFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
	394		POPOLIGAVTOPRIGGSRRNAMONG YAGLISOAISSADERRILT LAQIYENWAYTEYPENGEDONSAGARINSIERHISLHSKEIKV INBATGKSSUMMLNPEGGESGKAPRRRAASMOSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPUGHFAKWSGSPCSRIKEEDDWHTT FRERSSNASVSTRISPIRESEVLAEEIPASVSSYAGOVPT
	394		POPOTICANTOPRIGOSSRINAMENDS YAZLISÇAT ESA DEKERLÎN LAÇI YEMMENTYPETRUCHORSINAÇMINÎSTRINILA ELKEYLIN DENATUKSISHMENDE PROGUSSRINA ERMÎSTRÎNÎ ELKEYLIN DENATUKSISHMENDE PROGUSSRINA ELKEYBELÎNÎ ELKEY BERÇÎNÎ ELKEYATÎ PÎS DENATUSÎ SEÇÎNÎ ELKEZÎNÎ ÎNTÎ PÎ PÎ DES SÎNAĞÎ YÊ TÎLÊDÎ ELKEYBÎ SEÇÎNÎ ELKÎ YEŞÎ YAÇOVÊ PÎ ELKEYBÎ PÎ PÎ BÎ BÎ PÎ PÎ BÎ PÎ PÎ BÎ PÎ PÎ BÎ PÎ PÎ BÎ PÎ BÎ PÎ BÎ PÎ PÎ BÎ PÎ PÎ BÎ PÎ PÎ PÎ BÎ PÎ PÎ PÎ BÎ PÎ PÎ BÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ PÎ
			POPOTLOAVTOPRIGOSSRINMENDSYSTALLISQATESADERKIT, LAQTYTEMMENTYPETRUGENSSKYSKYMIKSTERNILSKHEKYTEV BREATVIGSSHHEIMPEGGISGRAPRERAANSOSSSKILGERSKA PRIKEPSGLAPPSFORHEIMSGSGCSERREEBENMET FERRESSNASSYSTRISFILEDESEVLAESTERSVSSYSAGOVPDT HARGIALIDAINTSSHILJERSGLOFSILEHSVSTYDFILTYSS SLPSPAROPLSAGGCTSSSQALEBALITSTDTPPEPADVIMTOVID FILOAPHTLALGOLDESSKLATGATOVICEPPERAFGSSLOPTI, SMLAPPPMGASPLERAGTFVLTIPPTERASCORNOCOLDIAVY MENLECOMORI ISOMADEGGESCHEPPIDPP
5995		2437	POPOTICANTOPRIGOSERINAMENDE YAZLISÇAT ESA DEKERLIF. LAQITYEMMENTYPETENCEDENS SAQMINISTERINISLEH KEYLEV INBLATUKSISHMELBERGICISGINA PERRALANDOS SIS KILLEGRESKA PEKKEPGGLAP PEKATYPES WELHANDISGINSCENS REBEZIMMET FEDRISSISMASIS VERTILGERE BEVLABET IRAVIS STACOV PPT FEDRISSIANDIS SISSE ASSENDATION OF ELECTROPIC PROPERTY PERSONAL DELIVERATION OF ELECTROPIC PROPERTY OF THE STACK OF THE
5995			POPOTLOAVTOPRIKOGSRINMENNENSYSTALLISOATISSADEKRITI- LAQTYTEMMENTYPYTEKUGENSKSJOKKUSTERINLISEKHEKYTEV RINEATKUSSHHILMPEGGISGKARPRAANSOSSSKILGERSKA RIKKEPGGIAPPSGVAHEKNOSGSCSTRIKEREEMIMTT FRENSSSKASSYSTRISFILRESEVILAESITSAVSSYSTAGOVPDT FRENSSSKASSYSTRISFILRESEVILAESITSAVSSYSTAGOVPDT FRENSSKASSYSTRISFILRESEVILAESITSAVSSYSTAGOVPDT FRENSSKASSYSTRISFILRESEVILAESITSAVSSYSTAGOVPDT FRENSICHTENSSKASSTATICHTENSIKASSTAGSTSLEREMONTHOTY FRENSIKASSTATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTSATICHTENSIKASSTAGSTAGSTSATICHTENSIKASSTAGSTAGSTSATICHTENSIKASSTAGSTAGSTSATICHTENSIKASSTAGSTAGSTAGSTAGSTAGSTAGSTAGSTAGSTAGST
5995			POPOTICANTOPRIGOSERINAMENDE YAZLISÇAT ESA DEKERLIF. LAQITYEMMENTYPETENCEDENS SAQMINISTERINISLEH KEYLEV INBLATUKSISHMELBERGICISGINA PERRALANDOS SIS KILLEGRESKA PEKKEPGGLAP PEKATYPES WELHANDISGINSCENS REBEZIMMET FEDRISSISMASIS VERTILGERE BEVLABET IRAVIS STACOV PPT FEDRISSIANDIS SISSE ASSENDATION OF ELECTROPIC PROPERTY PERSONAL DELIVERATION OF ELECTROPIC PROPERTY OF THE STACK OF THE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
10	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Godon ( manifold municipal de de de de de de de de de de de de de
	sequence	sequence	Codon, /=possible nucleotide deletion,
-	sedeence		\=possible nucleotide insertion)
1	i		ISDYFERRVEQPLYGLDGSAAKEATEEQSAL?TLMSVMLAKPRL
			DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
i			QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
			RQI\DBQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
			KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
			REZIERORKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
			TLAEYHEQEBIFKLRLGHLKKEEABIQAELERLERVRNLHIREL
	1		KRIHNEDNSQFKCHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
1	1		RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
1			YDYFSLDTDSFCTVLEYCBGNDLDFYLKQHKLMSEKBARSIIMQ
1			IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
			KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
			VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
			PKPVVTPBAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
			STSSPAGAAIASTSGASNNSSSN
5996	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
1	i		LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
	l I		AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWIQR/SWVSWRSRPGCE
1			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
1			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPF8
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5999	2	1790	RPPMEXARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
			GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
1 1			ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
1			LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
			QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
			ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
1.			FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
1 '			KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
1			QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
1			EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
			LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
1			VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
			LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
			TA\MSSWLSTFTTSTSQSLTE?PDEKP
6000	101	1561	TEPCRTAENCTATMSENNKNSLESSLEQLKCHFTWNLMEGENSL
1 1	,		DDFEDKVFYRTEFONREFKATMCNLLAYLKHLKGONEAALECLR
1 1			KABELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
1			VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
			ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
1 1			NQYLKVLLALKLHKMREBGEEEGEGEK\LVEEALEKAPG\VTDV
1 1			LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCOIGCCY
			RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
1 1			VCSILASLHALADOYEDAEYYFOKEFSKELTPVAKOLLHLRYGN
			FOLYOMKCEDKAIHHFIEGVKINOKSREKEKMKDKLOKIAKMRL
			SKNGADSBALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
			SWNGE
600L	1.76	1038	AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLOSSLITASOFFEI
			WLHFDADGSGYLEGKELONLIGELQQARKKAGLELSPEMKTFVD
	1		OYGORDDGKTGTVELAHULDTEENFLLLFPCOOLKSCE\ PEMKE
			QYGQRDDGKIGIVELAHVLPTEENFLLLFRCQQLKSCE\EFMKT WRKYDTDHSGFIRTERLKNFLKDLLEKANKTVDDTKLAEYTDLM

Deginning   nucleotide   location   corresponding   cotation   corresponding					
Molecution   Cocresponding   Cocation   Cocresponding   Cocation   Corresponding   Cocation   Corresponding   Cocation   Cocresponding   Cocation   Coca		SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
coation   corresponding					(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first maino acid residue of anino acid residue of anino acid residue of anino acid residue of anino acid residue of anino acid sequence control of acid sequence control of acid sequence	-	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of anino acid residue of anino acid an					H=Histidine, I=Iscieucine, K=Lysine,
amino acid residue of amino acid sequence amino acid sequence  Sectine, T-Threenthne, W-Valline, sequence  M-Tryptophan, Y-Typosine, X-Unknown, *-skt Codon, /-possible nucleotide deletion, V-possible nucleotide insertion)  LICLESEMBORICELTERMALLPUQUERFLIKEGETHICKEEP FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYTE FELTICORUNG ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYTA ILBERTLANDLOCKENROCHINTITYT HISTORICHINTITYT HISTORI	- !		to first		Debugine, M-Methionine, N-Asparagine,
maino acid sequence  amino acid sequence  ATTYPODEDILA TYTYTODIANA, STATUCANIA, SEQUENCE  EQUENCE  ACODON, PODGRIBLE MULICOCCIDE (SELECTION)  LICPOSRIBLE MULICOCCIDE (SELECTION)  LICPOSRIBLE MULICOCCIDE (SELECTION)  LICPOSRIBLE MULICOCCIDE (SELECTION)  LICPOSRIBLE MULICOCCIDE (SELECTION)  LICPOSRIBLE MULICOCCIDE (SELECTION)  ANALOGORY STATULAL LACAD (SELECTION)  ANALOGORY STATULAL LACAD (SELECTION)  ANALOGORY STATULAL LACAD (SELECTION)  BETTAL STATULATION OF THE SERVE MULICOCOLDINO DESIGNATION OF THE SELECTION					Securing Temporalise W. Weller
sequence  Codon, /=possible mucleotide disection, Vapossible mucleotide insection)  ILCESSMINGHEITERRELLPUQUERFILKFGGTFMCGKEFF  MASINGHIATERATULPUQUERFILKFGGTFMCGKEFF  MASINGHIATERATULPUQUERFILKFGGTFMCGKEFF  MASINGHIATERATULPUQUERFILKFGGTFMCGKEFF  MASINGHIATERATULPUQUERFILKFGGTFMCGKEFF  SANGASBULELDCOUTERBUYUNSBERICHGGGBGRMCHEST  BELFITERSEFWILLSFYTGHERIGERGRMCHLECTGAPFFFTM  EIKENRELLEGGV/UNIVERSERTERSTERSFWLECKAA  BENEFTISSEFWILLSYTIGHLEFTTP IPREFFFTCH-BITT  BEDFEARAFWANAVITTPHASENTHEITERSFWVLECKAA  BENEFTISSEFWANAVITTPHASENTHEITERSFWVLECKAA  BENEFTISSEFWANAVITTPHASENTHEITERSFWVLECKAA  BENEFTISSEFWANAVITTPHASENTHEITERSFWVMVERCH  ADTTSSHPMASKANAVITTPHASENTHEITERSFWVMVERCH  SELDEMARAVITTSSHERICHGLAKESANDLESGVVBRACT  HISTVICKNYFMERARALVITTPHAVPRAKVAATOCCAALFE  BENEFTISSEFWANAVITTRISSEFTANGERTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADDARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  PERMASANFANAFANAFANAFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIGHAM-VERTURGHTGADARFANAVITTRISTERSFWGRMSSANSANF  RIG					Waltrophan Y-Turneine Y-Unknown to Shan
Sequence    V-possible nucleotide insertion			amino acid		Codon. /whoseible muslectide deletion
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1 PARTITION OF STATE	-				

S30	Prodicted	Predicted end	Amiro agid coment contoled-not
ID	beginning	nucleotide	Amino acid segment containing signal peptid
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
101	location		Giutamic Acid, Fmpnenylaianine, G-Glycine,
		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding		L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	secuence	1	\=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPT
	I		RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR
	1	1	VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPR
		1	GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSI
			PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNE
	1	I.	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGOKEP
	l		IRALALKVLREILEHQPARFKNYAELTVMKTLEAHKDPHKEVV
			CARRAGOV LANGT CONCOUNT ON THE CONTROL OF THE CONTR
	i		SAEBAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQ
	l		KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVA
	1		HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDV
			GQS
6005	133	5955	RSSGRRQBQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDAL
		1	NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPK
		l	KRQKKERMLLCRQLGDSSGEGPEFVEEEEEVALRSDSEGSDYT
		1	GKKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAOL
	ŀ		EDWGMEDIDHVFSEEDYRTLTNYKAFSOFVRPLIAAKNPKIAV
	1	1	KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVT
		l	TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKP
	1	l	PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYS
	1	ſ	SDGSTSRSSRSRKKLRTTKKKKKGEREVTAVDGYETDHODYCE
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			CQQGGEIILCDTCPRAYHMVCLDPDMBKAPEGKWSCPHCEKEG
			QWEAKEDNSEGEEILREVGGDLEEEDDHEMEFCRVCKDGGELL
	}		CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKIL:
			WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGM:
			YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEE
			S\RKRKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDKK
			HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMR
			EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATG
			TLHPYQMBGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYS
			YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGD
			DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSY
			LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLWGYSLQH
			LLLTGTPLQNNLESLFHLLNFLTPERFHNLEGFLEBFADIAKE
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- 1			FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDSDWNPHNDIG
- 1			AFSRAHRIGONKKVMIYRFVTRASVEERITOVAKKKMMLTHLV
- 1			RPGLGSKTGSMSKQELDDILKFGTEELFKDBATDGGGDNKEGE
- 1			SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQYV
			REERMGEEREVEREIIKQEESVDFDYWEKLLRHHYEQQQEDLA
			NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDI
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			CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQE
1			
	ſ		LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVARHOAK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Tsoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, **Stop
	secuence	sequence	Codon, /-possible nucleotide deletion,
	seducince		\=possible nucleotide insertion)
1			QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME EVAEAAPQELDTIALASKKAVETDVMNQ\RQT\TLCRVPAGATG
	1		SLAPRPCDVPTCPTL
6007	3	2351	HELGOVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE
į.			GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK
1	1		EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSOLBYYAS
1			SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
1	1		FDSDRRRMSV:VQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
			HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALOOR\R
			EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV
			WVLTGDKHETAVSVSLSCGHFHRTMNILELINGKSDSECAEQLR
1	[ i		QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
í			LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
			GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
1			VQYFFYKNVCFITPOFLYQFYCLFSQCTLYDSVYLTLY\NICFT SLPILIYSLLEOHVDFHVLQNKPTLYRDISKNRLLSIKTFLYWT
1			ILGFSHAFIFFFGSYLLIGKDTSLLGNGQMFGNNTFGTLVFTVM
	i .		VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
			LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
			HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
			GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRCPAPEHAGPAR
			ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
1			DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNQDYRTKPFCCSACP
i			FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
1			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
1			KCTYRDPLYEIVRKHIYRRHFQHVAAPYIAKAGEKSLNGAVPLG SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG
1			HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
1			SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
i l			GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
			APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA
1 1			ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP
			AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
1 1			TFNDVEKMAAHMRNVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
			LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
l i	i i		TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYBQMEFPLLKKRKLDDDSDSP
			SFFEEKPERDALDAGE/EDDYSARARSFLTKYFT/KZPTP
	1		TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
			LGFNMKELNKVKHBMDFDAEGLFBNHDEKDSRVNASKTADKKLN
			LGKEDDSSSDSFRNLERESNESGSPFDPVFEVRPKISNDNPREH
			VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS
			EVDQDDVVEWKDGASPSESGPGSQOVSDFEDNTCEMKPGTWSDE
1 1	1	J	SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
1 1		J	QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP
6009	4272	1534	MHGSLAGVKLSSQQA
1	*****	*334	CHGLQHLTPFREINLSLQG*BPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW
	ļ		EAYTLGHQHWNWFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
		J	RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNOPGVMGLL
			NGKRGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG
1	ĺ		NCR:HIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
		j	VIQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
1			FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
			I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
l İ	1	1	AVTRCSAVQRRPSITISSIHVDTKIQQRLHDVMVAGADGVVQWG
		1	DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
		1	RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
			RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDELLWFGGR*LIIIG

SEQ Predicted Predicted end Amino acid segment containing	signal pentide
ID beginning nucleotide (A=Alanine, C=Cysteine, D=Aspa:	rtic Acid, E=
NO: nucleotide location Glutamic Acid, F=Phenylalanine	G=Glycine,
location corresponding H-Histidine, I-Isoleucine, K-L	vsine,
corresponding to first L=Leucine, M=Methionine, N=Asp	aragine,
to first amino acid P=Proline, Q=Glutamine, R=Argin	nine,
amino acid residue of S=Serine, T=Threonine, V=Valine residue of amino acid W=Tryptophan, Y=Tyrosine, X=Uni	
amino acid sequence Codon, /=possible nucleotide de sequence \=possible nucleotide insertion	
I**RGRLSGEWGC3LGRGELFQVSIGIGVS	
AGLVERGALHATGQGVEALVQQLLDVGPAG	
GRYGOLPAEGLQVCITLVAQWRMHDGRELGC	
CGVGGAILLKALSQYFLKGG*RLWCARGQ*1	
R*NGLTIHCFN*LI*GAVCCRLVILRWCGLI	
GSFPGRLWP*PFISQERPNGHCOWEFRLAV	
TWRYGNPLLNLL+GAWLGGAACGGQQGGFLS	TWQACTGPGQAAF
LPPFQGACRPRTQRCRTWVCPIAWRQLLAY	TRD
6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIE	
AGISQNAKTGDLPAFGECVGIASKALCGLTE	
PNSQAGHQGLVDPIQFARANQAIQMACQNLV	
TIVAKHTSALCNACRIASSKTANPVAKRHF	
VKTIKALDGDFSEDNRNKCRIATAPLIEAVI	enltafasnpefvs
IPAQISSEGSQAQEPILVSAKPMLESSSYL1	RTARSLAINPKDP
PTWSVLAGHSHTVSDSIKSLITSIRDKAPG	RECDYSIDGINEC
IRDIEQASLAAVSQSLATRDDISVEALQEQI IATAARGEAAQLGHKGTQLASYFEPLILAAV	ALSO A OR LOHD LOD
TVLDQTKTLAESALQMLYAAKEGGGNPKAQI	
BAVEDIMVTINRAASEVGLVGGMVDAIAEAN	
TPVDYQTTVVKYSKAIAVTAQHMMTKSVTNI	
YGHLAFQGQMAAATAEPEEIGFQIRTRVQDI	
ALQVCPTDSYTKRELIECARAVTEKVSLVLS	ALQAGNKGTQACI
TAATAVSGIIADLDTTIMFATAGTLNAENSE	TFADHRENILKTA
KALVEDTKLLVSGAASTPDKLAQAAQSSAAT	TTOLAEVVKLGAA
SLGSDDPETQVVLINAIKDVAKALSDLISAT	KGAASKPVDDPSM
YQLKGAAKVMVTNVTSLLKTVKAVEDEATRG	
3LTVFQSKDVPEKTSSPEESIRMTKG_TWAT	
DVIATANLSRKAVSDMLTACKQASFHPDVSE	
TLGYLDLLEHVLVILQKPTPELKQQLAAFSF EAMKGTEWVDPEDPTVIAETELLGAAASIEP	
PKQADETLDFEEQILEAAKSIAAATSALVKS	
VGSIPANAADDGQWSQGLISAARMVAAATSS	TORNANGREDVAGGR
SEEKLISSAKQVAASTAQLLVACKVKADQDS	FAMRRIORAGNAV
KRASDNLVRAAQKAAFGKADDDDVVVKTKFV	GGIAOIIAAOEEM
LKKERELEBARKKLAQIRQQQYKFLPTELRE	
6011 446 1835 LLQPANRKSPGLSDCLWAWILLLSTLTGRSY	GQPSLQDELKDNT
TVFTRILDRLLDGYDNRLRPGLGERVTEVKI	
DMEYTIDVFFRQSWKDERLKFKGPMTVLRLN	
FHNGKKSVAHNMTMPNKLLRITEDGTLLYTM	
GRDPPM\D\AHACPLKFGSYAYTRAEVVYSW	TREPARSVVVAED
GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTT	HFHLKRKIGYFVI
QTYLPCIMTVILSQVSPWLNRESVPARTVFG ARNSLPKVAYATANDWFIAVCYAFVPSALIE	
WDGKSVVPEKPKKVKDPLIKKNNTYAPTATS	
TIAKSATIEPKEVKPETKPPEPKKTFNSVSK	
GIFNLVYWATYLNREPOLKAPTHO	
6012 351 5013 PAELFQSFAIWHKELYDWRLGPWNQCQPVIS	KSLEKPLECTEGE
EGIQVREIACIQKDKDIPAEDIICEYFEPKP	
CIVSEFSAWSECSKTCGSGLQHRTRHVVAPP	
QVCQSSPCEAERLRYSLHVGPWSTCSMPHSR	
REKORSKGVKDPRARELIKKKRNRNRQNRQE	
EVMCINKTGKAADLSFCQQEKLPMTFQSCVI	
PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEK	ECPEFEEKEPCLS
QGDGVVPCATYGWRTTEWTECRVDPLLSQQD	KRRGNQTALCGGG
IQTREVYCVQANENLLSQLSTHKNKBASKPM	
QLCHIPCPTECEVSPWSAWGPCTY3NCNDQQ	
NBPTGGSGVTGNCFHLLEATPCEEPACYDWK	
BCGPGTQVQEVVCINSDGEEVDRQLCRDAIF	
CVLSTWSTWSSCSHTCSGKTTEGKQTRARSI NSSALQEVRSCNEHPCTVYHWOTGPWGOCTE	
NGEASCSVGMQTRKVICVRVNVGQVGPKKCP	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Asparic Acid, K=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1			
	corresponding to first	to first	L-Leucine, M-Methionine, N-Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLFAN
1			GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
1	ĺ		VQQDSP\GAQEGCGPGRQARAITCRKQDGGOAGIHECLQYAGPV
1	1		PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
i	1		KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
1	1		VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
	1		EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1	į.		GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWYTEPWSICKVTFV
1			NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
l			VCKLPCPEDCVISEWGPWTOCVLPCNOSSFRORSADPIROPADE
	1		
	1		GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
			KTRMLJCVRSDGKSVDLKYCRALGLEKNWQMNTSCMVECPVNCQ
1	1		LSDWSPWSECSQTCGLTGXMIRRRTVTQPFQGDGRPCPSLMDQS
			KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
1	1	1	DDFSKVVDEEFCADIBLIIDGNKNMVLEESCSQPCPGDCYLKDW
			SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
			ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
1			SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
			CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
			PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
1			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
1			ARPESNDCPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDRFMKEDFDVDHFVSDCRK
-			RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
	1		DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1			KKMCVLRLIQVIRSVEKIRKILNSQSSKRTSALRASSPLLTGOI
i			LERIATEFNQLQFHACQSK\GNPLLDKVRPRIAGITAMLOOSLE
	1		GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
			DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
			EKGNTVPGYDFLVNSVWPOIVOGLEEKLPSLFNPGNPDAFHEKY
			TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
1	l		EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
			IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
			ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
			ACVPSLSSKI IQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
1			SYVDSALKPLPQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
1			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
1			QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
	I		P
6015			
	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
	13	2237	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
	13	2237	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
	13	2237	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDNIVDLRHELT
2	13	2237	VKGKGSLPLSAHGIVVAMLSRAEWDQVTVYLPCDDHKLQRYALN RITUWRSRSGNBLPLAVASTADLIRCKLLDVTGGLGTDERELLY GMALVRPVALISERKTKPAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRGCYFVLDWLQKTYWCROLENSLEEIWBLEEFR
1	13	2237	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
	13	2237	VKGKGSLPLSAHGIVVAMLSRAEWDQVTVYLPCDDHKLQRYALN RITUWRSRSGNBLPLAVASTADLIRCKLLDVTGGLGTDERELLY GMALVRPVALISERKTKPAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRGCYFVLDWLQKTYWCROLENSLEEIWBLEEFR
	13	2237	VKCKGSLPLSAHSIVVAMLSRARKOVTVYLPCDDHKLORYALM RITYMENSRSGMEDLEVANTADLIRCKLUDVGGGLGTBELRLLY GMALVRFVNLISERKTKPAKVPLKCLAGEVNIPDMIVDLRHELT HKKNPHINDCRRGCYFVLDMIOKIYHCRGLENSLRETWELEEFR BGIEBEDGBERDKHIVVDOITEKÇHEPGDJGSSTESDVKADGDSK
	13	2237	VKCKSSI,PLSAKGI TVVAMLSBRAKDOVYVYLECDDEKLORYALM RITVBRBSGEREDLAVASTALLERKLLDVYGGLOTDEKLLLY GMALVERVALLSBREKTERAKVPLKCLAGDENI PRMI VDLHELT HKRMBHINDCRRGCYFVLDHLOKTYWCROLENSLRSTWELBSFR BGI BEBDGBBORNI VVDDI TERÇREHENDDGSKTESDVKANGUSK GSBEVDBHCKKALSHKELLYBRARELLVYSTESDFYVLAGELSK AZIKAWNESSFYCEVLABLKOVTCKRREKLVIDAFLDOGELVPT AZIKAWNESSFYCEVLABLKOVTCKRREKULDFLDOGELVPT
	13	2237	VICKOSI FLEANIGI VVAMLISRAKKOOVTYVIJE DDIKKLOPTALIN RTVWRSISSIANIEL LEVAASTABLI ISCKLILDIVOGGI DETEKLLIV GANLUPRINLIS BERTIFRATVELKELLAQIVATI DEN TVIDLERSLIT KROMPHINDERGOK EYVLOMLIGICHVICKOLLASI LISENBUGGETE BGI EREDDEBDINI VVOID ITBIÇKE PRODOCEST IS SIDVAGOGISK GESEVUSHICKALA ISKKLI KERSAKELIVAY ESSE OFTIVLEREYLIV KALIKANIM PSEPAVECULA ELKOVITCENE RAVIDA FLIDOEPLUPT FROILALLIGIET SERVIDLENDI VICKORI PSE ANTONIO PLODEPLUPT FROILALLIGIET SERVIDLENDI VICKORI PSE ANTONIO
	13	2237	VICKOSI-PLEANIGI VVAMLISRARKOQUTVYLJECDDHKLQEYALIN KITVINERSISSIALILLAVASTABLI (ICKLILLAVIOGI ETERLILLY GANLUK POMLIS BEKTEKANFELKELLAQURVIT DOKIVULLERELI KENDEHI DENGECE YVLUDILLOGI VETECLA BESIDEN ESSEN BEI EREDQIEDDRI VVDI I TEQUE PROGLOSI ESSENVARIOGISK KALIKANINE PROVEVULLE ALEKTORIE BENIDALI DODE VIVET PROGLAJALITEY EREVULLENDUL VETECHER BENIDALI DODE VIVET PROGLAJALITEY EREVULLENDUL VETECHER PROGLADI ETERGARER BALLEBMILLER DALI SIST ER PYTLERIVET LIVANT FERGARER
	13	2237	VKKKOSI-PLEANIGI VVAMILSPARKOQUTVIJLE DDHKLOGIVALIN RTVIMSRISSIMIL ELAVASTABLI DIKCILLIDIVOGI CIDERILLIY GMALVRPNILI SERTIFRATVELIKCILAQIVATI SENI TUDLERISLI KROMPHINDERGE VYEVLOBILOGIVAT PERCEDIS SILES PRIMILISER BGI EREDOBEDINI VVDDI TIBÇKE PRODOSET TISDIV KADODIS GESEVINSHICKALI SHEKKI TERRAKLIVY SESSE PITVLEREVLE KAITGANINNESPEVIS CULLEKOVITCENE RAVIDA FLIDOSELVET FROJALAJICI SEREVIDLADIVLIVENSOP SOPROFILISHI SONI FIC ALLEBHILSBL PALCI SGI REVITLERIVELI VARTETERNAREF SAQORBARROKELINGSAS ELDIR PROVINSCELOS CORREDULISTI
	13	2237	VICKOSI-PLEANIGI VVAMLISRARKOQUTVYLJPEDDHKLQUTALIN KITVINGKISSRALILLAVASTABLI (INCLIALID/TOGGI CIPERLLLY GANLUK PAVILLIS BEKTEKANVELKCILAQIWATI DOKIVIDLERELI, KKOMPHINDEGOG VYLUMLOKUTVENCOLLIS LIBENDEGET R BEGIERRODIS BORDI VVODI ITEQEPENDODIST ISDIVADIOGIS GERVOSICI SASI LIBENDEGO VICTORILLO YESING PILADERILLO GERVOSICI SASI LIBENDEGO VICTORILLO YESING PILADERILLO PICILALI LIBENDEGO VICTORILLO YESING VICTORILLO ALLEBMILSBEL PALI TOSI CHENTICA VICTORILLO YESING PILADERI SAGONISARRONELINICASI LIDERRIVIS CLIAS CUAS POLIBELI YKANGOGLIDAD SORKILLIC CITY TOSGENSILVOROS SASIPIO
	13	2237	VICKOSIELPEANIGI VVAMILISPARKOQUTVILJEODHKLQIVTALIN RTVWISSISSIMELLEVAAYSTADLICKLILDVOGGIOTERILLY GNALVRPNILISBERTIKRATVELKELLAQIVATI SENITUTELERILIT KROMPHINDERGECYVLOMILOGUTVERGELBESIBESTR BEITERSEDGEBURIVVODI TIEGEPENDDOSETTSSDVAGOGOSK GSEVUNSICKALAISHKILTERSARLINVYSESSE PTVLKEREYLD KALIKOMINSPERVSCULAELKOVTCENERSVLDAFLDOGELVPT KALIKOMINSPERVSCULAELKOVTCENERSVLDAFLDOGELVPT ALLEBHLSBLPALGISGI REVITLIKRIVIELI VANTKTERKARRF ROJALALGISTSERVOLDROWLVENSYSSICHSOVENSSENSSICH KROGGIKDARKOMINGSA SIDINFRYSSICLSSE VORSSENSSICH KROGGIKDARKOMVADASSISSISSISSICHOWSESSENSSICH KRYPTIDLIKAUTVASSISSISSISTORGOGOSKOONIVESSEKS  ESPITTLDILINVENSSISSISSISTORGOGOSKOONIVESSEKS
	13	2237	VICKOSI-PLEANIGI VVAMIJERARKOQUTYVIJECDDHELQIYAZI. IR RITVINBERSERIALILAVASTADLI ISCHLIALIVOGE TERRELIY GANLUR POMIJE BERTERARVEJEKELAQURVIT DORI VUELERESI. I REKURPHINDEGEROG YVIJENDI, GUTVERCOLLER SIE PREMIZE FR BEGIEREDO BEDDRI VVDID ITRIÇCE PRODUCET ESDIVADIO DE SALDAMINE PER ENERVIZIALI SIR SERG PUT LA PER DO POLITO SALDAMINE PER ENERVIZIALI DORI TERRE PUT LA PER DO POLITO SALDAMINE PER ENERVIZIALI DORI TERRE PUT LA PER DO POLITO ALLEBMISSI PLANTICI SICIPATI VIGINI PUT LA PER DO POLITO FRANCIO GENERALI SICIPATI VIGINI PUT LA PER DO POLITO FRANCIO GENERALI SICIPATI VIGINI PUT LA PER DO POLITO FRANCIO GENERALI SICIPATI VIGINI PUT LA PER DO POLITO FRANCIO GENERALI SICIPATI VIGINI PUT LA PER DE POLITO FRANCIO GENERALI SICIPATI VIGINI PUT LA PER DE POLITO FRANCIO GENERALI SICIPATI VIGINI PUT LA PER DE POLITO PUT LA PER DE POLITO PUT LA PER DE POLITO PUT LA PER DE POLITO PUT LA PER DE POLITO PUT LA PERE DE POLITO PUT LA
	13	2237	VICKORSI-PLEANISI VIVANLISPARKOQUTYUJE-DDHKLOGYTALIN TYUWRISHOSHI LEIVAAYSTALI LICKLIJAUTOGGI DETERILLY RANDHI LORGENE VERVANISHI LICKLIJAUTOGGI DETERILLY RANDHI LORGENE VYALDINI, OTI VIVEKOLIBIS IR EN PHILLESPA RANDHI LORGENE VYALDINI, OTI VIVEKOLIBIS IR EN PHILLESPA GREVORICKALSHKALI TRARRELLIVI SESSOPTIVLE KERVLIJ RATKANINNES PAV VIVALBELAVI VICENS REVILDAT LORGENIST FROM LANDHIN SEN VIVAL LIGHTANISH VILLIAUT TERRORREF SAGOWARNISH LORGENIST LORGENIST VILLIAUT TERRORREF ALBEMBERS PAN VICALBELAVI TI VISASSELIVORISMI SEN LORGENIST TAMMO LORGENIST LORGENIST VILLIAUT TERRORREF TAMMO LORGENIST LORGENIST VILLIAUT TERRORREF EKRALDOVERSENIST LORGENIST VILLIAUT TERRORREF EKRALDOVERSENIST LORGENIST VILLIAUT TERRORREF EKRALDOVERSENIST LORGENIST VILLIAUT TERRORREF EKRALDOVERSENIST LORGENIST VILLIAUT TERRORREF EKRALDOVERSENIST LARGENIST VILLIAUT TERRORREF EKRALDOVERSENIST VILLIAUT TERRORREF E
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ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Coden ( managed and a series of the series o
1	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
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			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
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		l	RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
1			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
	}	j	GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
			FLPPKGWENEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
1 1			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
[			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1			LTQTASSTAGAMRELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
1 1		!	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1 1		1	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1 1		1	YAHICFLHRSKTTBIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1 1		,	NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
		İ	HPVMNGDKACGDVLVTARLILRGKDGSNLPILPPQRAPNLYMVP
1			QGIRPVVQLTAIBILAWGLRNMKNFQMASITSPSLVVECGGERV
1 1			ESVVIKNLKKTPNPPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
$\Box$			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
	1		DWWSKFYASSGEHEKCGQY1QKGYSKLKIYNCELENVAEFEGLT
		ŀ	DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
1			RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
1			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1			NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
1 1			NKQKTOVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
			SIDQTEFRIPPR\LIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRFETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LPVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	EATQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
1			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
			RKLRSRSLSQTHEAAVRMRSEATDVKSTLABIEDWLDKLMQLTB
			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
			GKTQTIFLKYPQBKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYONESRYP
1 1			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
i i			AVDEKGWEYGITIPPCHKPKSWVAAEKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOKHSA
			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1 1			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPOTVLO
l i	1		NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
ļ I			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
i I			QGIRPVVQLTAIEILAWGLRNMKNFQNASITSPSLVVECGGERV
f 1			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
l I			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
			DIVIENEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
			DWSKPYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFEGLT
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1			KKVIE\DROHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
			TFTRDBKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFOP
			NIS\RYYLRVIIWNTKDVILDRKSITGEEMSDIYVKGWIPGNEE
			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
- 0			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
		i	PCYAEKDGARVMAGKVEMTLEI LNEKEADERPAGKGRDEPNMNP
i			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
6023	102	916	LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQBLGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
	1	J	SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF
			LEGL/IVCSGR\VFQAQKEPHPLQFLREANAGNLKPLFEFVREA LKPVDSGEARWTYPVLLVDDLSVLLSLGNGAVAVLDFIHYCRAT
	1		VCWELKGNMVVLVEDSGDAEDBENDILLNGLSHQSHLILRAEGL
			ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
	i	ļ	AKGMSPAVL
6024	3	3260	FLSFLCYPRFRCLFCLQFATPASRMEQLNELELLMEKSFWEEAE
	1		LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVONKEGNCEK
			RLVITASQSLENKELC:LRNDWCSVPVEPGDIIHLEGDCTSDTW
			RLVITASQSLENKELC:LRNDWCSVPVEPGDIIHLEGDCTSDTW IIDKDFGYLILYPEMLISGTSIASSIRCMRRAVLSETFRSSDPA TRQMLIGTVLHEVFQKAINNSFAPEKLQELAFQTIQEIRHLKEM

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:			(A=Alanine, C-Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	SwSerine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	ded-
	secuence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	1		YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPQMQLSL
	1		PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKLDVTVGVKI
			HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP
1			EAGLLLYLKTGQMYPVPANHLDKRELLKLRNQMAFSLFHRISKS
			ATROKTOLASLPQIIEEEKTCKYCSQIGNCALYSRAVEOOMDCS
i .			SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN
			HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH
l l	J	l	
1			GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
1	I		RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR
1	1		DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
	I		VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
1	1		AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
1	I	1	KS\LALLEELYTSQLIDATTCMGINHPIPSRKIFDFCIVDEASQ
1	1		ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
1	i		KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA
1	1		NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD
1	1		KVPAPEQVEKGGVSNVTEAKLIVPLTSIFVKAGCSFSDIGIIAP
	1		
	1		YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN
	,		KDGTVGELLKDWRRINVAITRAKHKLILLGCVPSLNCYPPLEKL
6025			LNHLNSEKLI IDLPSREHESLCHILGDFQRE
6025	3977	89	GGFFAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
	l .		ARYGEAGEGPGWGGAHPRICLQPPPTSRTSFPPPRLPALEQGPG
			GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVQQWVSYADTELIP
!			AACGATLPALGLRSSAQDPQAVLGALGRALSPLEENLRLHTYLA
	!		GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ
1 .			PEFRAVLGEVVLYSGARPLSHQPGPRAPALPKTAAQLKKEAKKR
	1		EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVITYDLPTP
			PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
J	!		AANPRGVFMMCIP>PNVTGSLHLGHALTNAIQDSLTRWHRMRGE
1			TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
			KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR
1 1			
			LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG
			YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV
1 1			HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT
1 1			PAHDONDYEVGORHGLEAISIMDSRGALINVPPPFLGLPRFEAR
!			KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPCWYVR
i	i		CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
1 3			KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE
1 1			KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED
1 1			LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
1 1			IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS
			EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQCRDINLDVN
1 1			
			RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR
[ ]			WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC
1			LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ
1 1			RLPRRMPQAPPSLCVTPYPEPSECSWKDPEARAALELALSITRA
			VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG
	1		QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP
1			ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E
	1		VQEADEAKLQQTEAELRKVDEAIALFQKML
6026	2674	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVOAVDKKVDCPRLC
1 1	1	J	TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ
	ı		TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
, ,			YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLEN
	i		
	ĺ		
			LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK
			LLRLHLINSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH
			LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDINKNPINRIRRGDFSNMLHLKELGINNMPEL
			LLRIHLMSNRLOMINSKWPDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENDESISFYDNRLIKVPH VALQKVVNLKFLDINKNPINRIRGPSNNLHLKELGINNMPEL ISIDSLAVDNLPDLRK_EATNPPRLSYIHPNAFFRLPKLESIML
			LEKLHANSNELONINSKYPDALPNIESILMIGENPITETENMERK PLINIKSLVIAGINITETEPONALVELENESSESTEVENELKUH VALOKVVNLKFLDINKSPINRIRRGDPSNMLHIKELGINNMPEL ISI DELAVDRIPDIEKTEATINDERLSYTHUNAFFRIEKLESILMI KNALSALVHETTESIPMIKETS ISTENDER TOCOVIRMINNETIN
			LIKLHAUSHKLOMINKKWFDALDNI.EILHIGSNEYITLIKONEYK DLINI.ESLYVAGINLTE! DENALVGIENLES IS FYDNELLSYH VALGKVVNLKFIDI.NKDEPINNI NRGDSENNILLIKEIGIINNEBL ISI DELAVDNIDDJI.KE CHAINFREST HIENSPERIJKEIGIINN KSNALSALYHOTIESL.PHILKEISI HISNEI ICCUTIRNINMEKTI HERMEPDSJECUTOPEPGGGGOKWOVHPROMBICILLELIAPESEP
			LEKLHANSNELONINSKYPDALPNIESILMIGENPITETENMERK PLINIKSLVIAGINITETEPONALVELENESSESTEVENELKUH VALOKVVNLKFLDINKSPINRIRRGDPSNMLHIKELGINNMPEL ISI DELAVDRIPDIEKTEATINDERLSYTHUNAFFRIEKLESILMI KNALSALVHETTESIPMIKETS ISTENDER TOCOVIRMINNETIN

SEŌ	Predicted		
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D-Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KFYVHSBGTLDINGVTPKRGGLYTCIATNLVGADLKSVMIKVDG
			SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
			TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
ł			KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
			CLSPEMNCDGGHSYVRNYLOKPTFALGELYPPLINLWEAGKEKS TSLKVKATVIGLPTNMS
6027	5254	4148	
			GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSORPRT
ĺ	i		LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
			TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
!			QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1			TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
			FTNYNWREEHLERMLGQAGERRADVYVGVDVFARGNVVGGRFDT
	ļ.		DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
			DPVALRNRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
			LNVHMEVCAAFEAKEETYKSLMQKGQOMLARCPKSAETNIDODI
			NNLKEKWESVETKLNER\KT\KLEEALNLA\MEFHNSL\ODFIN
			WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREQII
			BLDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVVQRLVERGR
1	J		SLDDARKRAKQFHEAWSKLMEWLEESEKSLDSELEIANDPDKIK
			TOLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
			DMLSELRDKWDTICGKSVERQNKLEEA\LLFSGQFTDALQALID WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ
ł			ALKRSARELIEGSRDDSSWVKVQMQELSTRWETVCALSISKOTR
			LEAALRQAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT
	,		LIDOHKEFMKKLEEKRABLNKATTMGDTVLAICHPDSITTIKHW
			ITIIRARFEEVLAWAKQHQQRLASALAGLIAKOELLEALLAWLO
	1		WAETTLITOKOKEVIPQEIBEVKALIAEHQIFMEEMTRKOPDVDK
i I			VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSOT
i			QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA
1			NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
			GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
i			YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
	1		FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
			NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
			SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
			BCSDFPVPSABGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA
			ARVRTOFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPORKSPASK
			LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCTESVMENSKVLGESM
			AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
	i i		VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
i			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
			PTWSVLAGHSHTVSDSIKSLITSIRDKAPGORECDYSIDGINRC
- 1	i i	ľ	IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
- 1			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITBAAQLMK
ļ		J	EAVDDIMVTLNEAASEVGLVGGMVDAIABAMSKLDEGTPPEPKG
i			CFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
			YGHLAFQGQMAAATAEPBEIGFQIRTRVQDLGHGCIFLVQKAG\
	1	1	ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
- 1			TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
1		- 1	KALWEDTKI LUGGAAGTEDET AOAAOGGAATTTOI ATTENTO ATT
			KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SIGSDDPRTOVVLINAIKDVAKALSDLISATKGAASKEVDDDCM
			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALBATIBCIKO
			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			TLGYLDLLEHVLVILQKPTPBLKQQLAAFSKRVAGAVTELIQAA
			BAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
1			PKQADETLDFEEQILEAAKSIAAATSALVKSASAAORELVAQGK
			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
			SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
			LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
1			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
			TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
1	1	I	SYLVFNVIPTLADIIIGIIYFSMFFNAMFGLIVFLCMSLYLTLT
			IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
	i		VERYREAI IKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
1			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
1			MEMMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
			BTLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
1			RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
	1		AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
1			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
ì			IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADNW
			QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVECADEALQKAIKS
			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
		!	DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
		!	IKLVGBIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
1			DISKLAEFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFREIFSV
			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
			FVTQWLKEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
			YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
1			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
1			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
1			IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
			KFARLVNYNKMVFCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
			SCDRIKEEFOFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
			QVTMABLWAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
			PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
			SVSPSASFRGAEKHRNSADYSSESKKOKTEEKEIAARYDSDGEK
1 1			SDENLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
1 1			ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAAYGRSPVVGFD
			PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQNQPVPFPPDAL
1 1			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1 1			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1 1			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1 1		· i	W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
1 )			EVLHVTKPDKYQLHLH3SCVLSLKFAHCGKWF\VSTGKDNLLNA
1 1			W\RTPYG\ASIF\QSKRSSS\VLSCDI\SVDDKYIVTGS\GDK\
			RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
	j		SCDRIKEEFQFLQAQYHSLKLECBKLASEKTEMQRHYVMYYEMS
1 1		1	YGLNIEMHKQAEIVKRLNAICAQVIPFLSOEHOOCVVQAVRRAK
1 1			QVTMAELNAIIGOQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
1			PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHCRDRDSIKSS
1		J	SVSPSASFRGAEKHRNSADYSSESKKOKTEEKELAARYDSDGEK
1 1	ļ	J	SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
1			ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	aminc acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 -	\=possible nucleotide insertion)
			MNGRLTSPGAAYAGLHNISPQNSAAAAAAAAAAAYGRSPVVGFD
			PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
1			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FPTSPVFSLGYCP\TEEWLAVGMENSN\V
1			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
			W\RTFYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
		ĺ	RATVYEVIY
6034	2683	714	<b>E</b> SGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPRERAAAAM
1			BIAPQEAPPVPGADGDIERAPARAGSPSPASPPADGRLKAAAKR
			VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
			RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCRALEEVFKR
1			LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
i			LAVLHLENASLSGRPIMLLATALKMNMNLRELYL\ADNKLNGLQ
			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICRGLKRORKGI.
			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
			RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
1	1		DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
			TQKALLABIQNGCKRNLVLARBREEKEQPPQLSASMPETTATEP
			QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDGEEEEEERGERDET
	l		PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP PPGPEVKGGSCGLEHELSCSKNEKELELLLEASQESGQETL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
			YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
1			LENASTLALPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLORN
1	1		SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
1			VLRAALDSGAFQSVWVSTDHDEIENVAKCFGAQVHRRSSEVSKD
İ			SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR
			EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGBLYENGSFYFAKRHLIENGYLOGGKMAYYENRAEHSVDIDV
			DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
1	ĺ		GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
			LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
			RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFARHIC\LL
			MEKGLINFMPKNRNLAVNIGEKK
6037	2936	1919	WISWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
			GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR
			SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHBLRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
į l			HNAEERRALAGARDLSADRPRIGHSFSFAGFFSAAATAAATGLL
			DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
			PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
			SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALOBFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
			YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS
		1	SDKTDGTAGTPAISTTTTVEIRKSSVMTTSITSKVEKSPTTATG
			NSSCPSTETEEEKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
			TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD
			VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
			AATLFQTSALPPALLRPAPGP:RTAHTPVLFAPY
6039	4073	1000	LDEYEARLTLANLDDFEEUNEDDDENRVNQBEKAAKITELINKL
l i			NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSERPITETASP
	l i		RKTEDSFYNNSYNPFKEVQTPQYLNPFDEPEAFVTIKDSPPQST
			KKKNIRPVDMSKYLYADSSKTEERELDESNPFYEPKSTPPPNNL
			VNPVQBLETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVNCKEVTKNYRGVKITNFTTSW
			RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
i		l	SRLLEPSDMVLLAIPDKLTVMTYLYOIRAHFSGOELNVVOIREN
		I	SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
1			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
		1	SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
			ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
1			LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
İ		İ	SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL LBQARRDAALKAGNKHWINTAAPFCNRQLSDQQDEERRROLRBR
1		Į.	ARQLIABARSGKMSELPSYGERAAEKLKERSKASGDENDNIBI
1		ĺ	DINEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLE
i			VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
			RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
1			EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEOKO
			IDTRAALVEKRLRYLMDTGRNTEEBEANMOENFMLVNKKNALTR
			RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTBAQKRRE
1			QLLLDELVALVNKRDALVRDLDAQEKQAEEEDEHLERTLEQNKG
6040	475	1052	KMAKKEEKCVLQ
	1//	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
1			LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
			LDAHTWIKSCRPIIRPNSGFWEQLIHYEFQLFGKNIVHMVSSPV
1			GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
1 1			NLLQVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
			EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
			VNERKSEQHLRFLSTLLDSFSSSRVPKMLLGDEKQSIVQAKPLE
			IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
i .			DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWILLSLVLSQ
1 1			HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
1 1			CK_KNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
1 1			DINSLQVLLSAVDDLLNTLLESEDSYLNGVYIGSVMPNDSEWBK
1			MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT
			SALLSKMVLIALRKETVLENNELEKITAELLYSLOWCEELDNPP
			IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
J J			SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
1 !			FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
1 1			TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
	I		NIBIIRFLSLPLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
	1		BFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPNCETLTY
	1		ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
1 1	1		VQIAVYHMLYKLMPBLPQYDQDNLKSYGDEEEEPALSPPAALMS
1 1			LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
1 1	1		LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR
1			TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL
			KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT
	I		STOLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
		ļ	IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
			VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
6042	1306	253	KWFTSSNKSTCSLCRETFF
*****	2300	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVROVSLTYP
1			GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
			GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHODWEV
- 1			QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
	1	1	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL
			GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK
			The state of the s

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SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			II.ADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
6043	403	599	LCLFFFFFCATPVLPLPSLISAL/CLSHLSVSSWFCFCQPPLPC
1			PLPPLQNKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQOVRHSLLGYLGVVV
1			DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
İ	1	1	AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMIDLQRPQPPPPPPPG
			AHSPGATPGPGTATAERSSGVAPAASFAAPSPGSSGGGGFFSSL
			SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT
			DWAKYFKGKKIHGEIDIKVBQABFSDLNLVAHANGGFSVDMEVL
			RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
			VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
1	ļ.		EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
1			KTYATAEPFIDAKYDVRVQKIGQNYKAYNRTSVSGNWKTNTGSA
	1		MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
			VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRORORDASPGR
1			GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP
			QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
			ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
1			ATROTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
Į.			AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
1			AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKARTTRS
1			LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
			SLIMDSPRAGTHOGPLDAETEVGADRCTSTAYORORPOVEOVGK
			QAPLSPGLPAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVTVQCA
			FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
[			WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
			SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
			VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
			KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
			IEEKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN
1			LKDBEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
			INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
			NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
i			HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
			TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1.0			WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\BASRESSKPRAV
1			LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
			TNNLYIFQDKVNSDMH
6043	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
			KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
1			ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1	1		EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1	1		SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
1			PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
	1	J	DGPSVMDRTSNDAFDSLERKCMBKEKCKKPSSLKPEKIPSKSLK
1	1		SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
	į.	ļ	NSPQLEPIQPEPTVMGEPFTVNPALTPAKDKKKEKKKKKESSKE
( I	1		LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
			LASIKABADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV
			TONGARASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDABQLVK
			EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
	1		AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
1 1	ľ	1	YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP
1 1			TLTKAPSLTDLVKSGPGKAKEPGADPAKSVI IPKLDDSSKLPGQ
1 1			APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA
L			EPRMWTYVYPAKYSDIKSEDERNKEERDRKLKEERSRSKDSVPK

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SEQ   Predicted   Predicted en   Intio acid segment containing signal p   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, Debaparic hoise   (AwAlanine, CaCystein, CaCys	, E= ne, Stop PHQSY YSFSP HYKSK DRPRT ASQQG
District   District	Stop  QHQSY YSFSP HYKSK DRPRT ASQQG  ESSAT
Corresponding   Correspondin	Stop QHOSY YSFSP HYKSK DRPRT ASQQG ESSAT BSAGS BYRMV
Corresponding to first amino acid residue of emino acid sequence   Section, Tentronine, Wealine, Section, October 1988, Section, Tentronine, Wealine, Section, Section, Tentronine, Wealine, Section, Section, October 1988, Section, Tentronine, Wealine, Section, Section, Tentronine, Wealine, Section, October 1988, Section, Tentronine, Wealine, Section, Section, October 1988, Section, Tentronine, Wealine, Section, Section, October 1988, Section, Tentronine, Wealine, Section, Section, October 1988, Section, Tentronine, Wealine, Section, Section, October 1988, Section, Tentronine, Wealine, Section, Section, October 1988, Section, Tentronine, Wealine, Section, Se	QHQSY YSFSP HYKSK ORPRT ASQQG ESSAT BSAGS
### smino acid residue of amino acid sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence solvente sequence se	QHQSY YSFSP HYKSK ORPRT ASQQG ESSAT BSAGS
residus of emino acid sequence Codon, "Popusible nucleotide deletion, Codon, "Popusible nucleotide deletion, Codon, "Popusible nucleotide deletion, Codon, "Popusible nucleotide deletion, Codon, "Popusible nucleotide insertion EDMERGISEDELL'SERSELESESESESESESESESESESESESESESESESES	QHQSY YSFSP HYKSK ORPRT ASQQG ESSAT BSAGS
omino acid sequence   Codom, /~possable nucleotide deletion, /~possable nucleotide deletion   Possable nucleotide deletion   Possable nucleotide deletion   Possable nucleotide deletion   Possable nucleotide deletion   Possable nucleotide   Po	QHQSY YSFSP HYKSK ORPRT ASQQG ESSAT BSAGS
cemano acid sequence Codon, /=possable nucleotide deletion, sequence EDKMSSTSSDCMLPTSSUSKLESKERPSSWTYPSSULT    EDKMSSTSSDCMLPTSSUSKLESKERPSSWTYPSSULT    IPHNIGIS VS.GSJDOPHNISTSRDSMANDAMSTOPPUSFLESS    YGSKVGGGEDADKARASSSVTCKSSSESKALDILGGERS    STIENTINGERBOOLOVGGGGSSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGGGSSVGVGASGAGGGSSVGVGASGGGSSVGVGASGGASG	QHQSY YSFSP HYKSK ORPRT ASQQG ESSAT BSAGS
EPGREGYESDE/LEPSEUSE/LESKEEPSESWIPYSS/LESKEEPSESWIPYSS/LESKEEPSESWIPYSS/LESKEEPSESWIPYSS/LESKEEPSESWIPYSS/LESKEEPSESWIPYSS/LESKEEPSESWIPYSS/LESKEEPSESWIPSES	YSFSP HYKSK DRPRT ASQQG ESSAT BSAGS
I PYMINGY SYSGAYDPHISTREMPAYMAUNTPOSYLEGS YGGKYAGGENADARARASPYTYCKSSESKAULDIVERSE YGGKYAGGENADARARASPYTYCKSSESKAULDIVERSE SPITADHTSQRADGGOCOVQQQQGSCSYQQAQQQBSSTAV SYSGAYDA SYSGAYDRADGGOSSYADAQQBSSTAV SYSGAYDA S	YSFSP HYKSK DRPRT ASQQG ESSAT BSAGS
YGSKYSGGENADEANASPSYTCKSSESSKALDILOGENS SPTISHISEGENEROCOVYCKSSESSKALDILOGENS SPTISHISEGENEROCOVYCKSGSESSKALDILOGENS SPTISHISEGENEROCOVYCKSGSESSKALDILOGENS SPTISHISEGENEROCOVYCKSTALD STEELT PROTESTALD STALLING SPTISHISEGENEROCOV SPTISHISEGENEROCOVYCKSTALD STALLING STALLING STALLING STALLING STALLING STALLING SPTISHISEGENEROCOV SPANNEROCOSSELLAND STALLING STALLI	HYKSK ORPRT ASQQG ESSAT BSAGS
SPITABRYSQUEDMOCCOVYGGGGSCSS VGGAGGGSCSS SPGAGGGGSCSS SPGAGGGGSCSS SPGAGGGGSCSS SPGAGGGGSCSS SPGAGGGGSCSS SPGAGGGGSCSS SPGAGGGGSCS SPGAGGGGSCS SPGAGGGGSCS SPGAGGGGGAGGGSCS SPGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ORPRT ASQQG ESSAT ESSAGS EVRMV
SSEGMANTHHERHICATSLLDAQYNLDYAAGILSETAIV STESILYEPER SGEDERAPHINEGORSETLE 1089 MYGYFERRYES IRSGEDERAPFORSAYHHESGREFTLE NESYYESTOOLAGUSCESTEASYG\KALABYOYOYHOWA YPAKARADYSYASSYRIQYGGAYHEVBANTYGERVYYS NORTHAYRERYTISS FOLABAGREYCKYTIALEERAE GULTOVKUTFONGUSIKK IMINOSERYEPERSSESSEN NORTHAYRERYTISS FOLABAGSTIK KANADERYDERKYYSIS OLDOVKUTFONGUSIKK IMINOSERYEPISSESSENIKA ASSINISHAPPOSICADILAGSTIK ASSINISHAPPOSICADILAGSTIK FOLABAGSTIKANTA FOLABAGSTIKANTAA	ASQQG ESSAT BSAGS EVRMV
6049 215 1089 AMTGYFEREYPEREX GEOFGAFFOTSAWHHESGESFTLE DSPYYSFOGARHGYCSFTSASYG\KALBYFOYGYHAY YFAAXAADYSYASSYTGYGGARHGYCSFTSASYG\KALBYFOYGYHAY NGEFEKVREPTITSSFGLAALGARFOKTOYLALPESBAF GLATOTOVERHPONRSKHIKENINGENPEBISSFGLAALGARFOKTOYLALPESBAF GSPAWEPGGSSRILSHHPARBYFTSAGDFASYLENSA ASSINSHLAPPOSAGBFILSHGFATAGG FYANKSYLVALWASSGSGKTSKRSITFARTAGGAFTGG FYANKSYLVALWASSGSGKTSKRSITFARTAGGAFTGG FYANKSYLVALWASSGSGKTSKRSITFARTAGGAFTGG FYANKSYLVALWASSGSGKTSKRSITFARTAGGAFTGG FYANKSYLVALWASSGSGKTSKRSITFARTAGGAFTGG FYANKSYLVALWASSGSGKTSTARYSVLITVOYGASELE DCGGGTFFARWFTSGBNIFFGCART	SSAT SSAGS VRMV
6049 215 1089 ANTOYFERENTSIESSEPPOTSANATHISSESSEPPO DESYYSFORDANISCESTRASON (ALBENDOVICHOWN YPANAMADESYASSYNDYMONOMINUPSANTHOPERSYTS NORTHANKERPTINSSPOLATION (ARRENDOMINUPSANTHOPERSYTS) OLIVOUVICHIPOKROSKI KKIMINOMEN PERIBSESSIPPO GENAMBED/OSSRELIMBINISMENTINSSPOLATION GENAMBED/OSSRELIMBINISMENTAL PROPRIESSESSIPPO GOSTAMBED/OSSRELIMBINISMENT (ARRENDOMINUPSANTHOPERSING) FUTANKEN/LUMISSISSIPPOSICIESTI (FARVILLADISSIPPOSICIESTI (ARRENDOMINUPSANTHOPERSING) RIBIOLIUS SLETTSINDSVORTETEVERSINGREGUE DOCOOLOPPISMENTSCHIMBINISMENTAL ILLIANDISMENTAL DESCRIPTION OF THE PROPRIESSIPPOSICIESTI (ARRENDOMINUS ARREND	SVRMV
DSTYPESTOLARICATES PERSONAL MALINET SHAPE PLANT PRACATALLY SASSATURE AND ANALOG SHAPE PRACATALLY SASSATURE AND ANALOG SHAPE NGEPEKVERPETTES FOLIALIQEERO EVIL ALE SEASE GLIOTOVENTHEROMERS HE WITHOUGH PERSONS PLANT GS PAWE POSSPELSHEP LAMPOT SASSATURES ASSISTENT PROSCRIPTION OF THE PROSC	SVRMV
PPAKAYADYSYASSYNGYOGANINVPSANTOPERKYYSS  NGEFKEVEREPTISSFORJAGIKSPENTYTALPERAE GIJTOTVKLIPFONERSKI KKIMKNERVPERISSSSSING GSTAVMETOPERSSKILSHIPMANTYSKOEDASSTINGS GSTAVMETOPERSSKILSHIPMANTYSKOEDASSTINGS GSTAVMETOPERSSKILSHIPMANTYSKOEDASSTINGS GSTAVMETOPERSSKILSHIPMANTYSKOEDASSTINGS GSTAVAKTIVALUMINGSSGKITSKENSKI TARMYLAGHEN FILISLOIMSSLSTYSLOPSVORTEFETVERSHIPMALUM DOCOGOPPHENSYTSGENIER TARMYLAUTVERSELLE	SVRMV
MORFRAVERPRITES FOLDALOGREPOKTOVIAL PERSENDE  OLTOTOVIKHPORNERS IK KINNEMP PENSES PASSANDE  OSPANWEPOSSERLSHHPURAPPTSNOS PASSANTERSA ASSINSHLAPPOSOLOPILALAGSTLY  FOLDS  F	NEWN
GLTOTOVKLIPFONRSKIKKTINKSENPPERISSSSIPMS GSTAVER-FORSSSILSHIPMSALSTIKV GSTAVER-FORSSSILSHIPMSALSTIKV ASSISSILLIPPSSALSHIPMSALSTIKV TO SEE  1718 FINANSKIVILLINGSSISSSSILSHIPMSALSTIKV FINANSKIVILLINGSSISSSSISSILSHIPMSALSTIKV RIHSLOTUSSLISTISTUSSVORTKETEVERSHIPMSALSIL DOGGOTPHSKIPTSGENLER FANNSVALTIVETVESSELLER	
GSPAWEPGSSRILSHHPHARPPTSNOSPASSTIRNSA ASSINSHIPPOSOLOPILAINGSTLY 6050 566 1718 KGLERTCCHMESNSKTYTEKEN-GDPHOPPLGEPGTGS PUTAMKKNYLJAKSSOSKTYSKENSIJFANYLJAGOTG RIHSLOIMSSLSTYSLVDSVGHTKTFUSHSHVRIJGU DCGGOTPHARPTSCRADHIFAVSVLITVPOVSKRILE	CONCE
AASSINSHLIPPOSLOHPLALASCILY  6050 566 1718 KGLERTCCHEESDSKTTEREN.GPEN.PPIGEPCYGS PWTAMKKYVLIMOKSOSGKTSMRSI I PAHYIAGDTRIG R HASIQINSSLSTYSIVDSVOHTKTEVERSHVREJOHL DCGGOOTPHENEYPTSGENLIFERWYWLIVEVOHYSERLIK	MANAGE
6050 566 1718 KGUBETCCMMESDSRETTEKEN/OPPUNDPFJGEFOYGS PRITAMKEN/LIMKSOSGSTRENS I I PARTIVADTRILG RIBIO/INSSLSTYSI/MOSVANITETEVERSHVRFJGMI DCGGOTPHENFERGRANIFERRIVALITY JERNEN/LY LYDVISSRELE	millo
PNTAMKKIVLLMCKSGSSKTSKRSII PANYIARDTRRLG RIHSLQINSSLSTYSLVDSVGMTKTFUVEHSHVRFLGRLI DCGGQOTFMENYFTSQRDNIFRNVSVLI VYVPUSSBELE	GWVT.
RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNL DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELE	OTTT.
DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELE	LNLW
	DMHY
YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKBR	EDLR
RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVCQLE	NLRN
FAEITEADEVLLFERATFLVISHYQCKEQRDAHRFEKIS:	IIKQ
FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVM.	DPSI
PSAATLINIRNARKHFEKLERVDGPKQCLLMR 6051 566 1718 KGLERTCCAMRESDSEKTTRKENLGPRHODDLGERGVGS	
6051 566 1718 KGLERTCCAMBESDSEKTTEKENLGFRMDPPLGEPG\GS: PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLG;	.GWVL
RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNL	TILL
DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELE	
YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKERI	EDILE
RLSRPLECSCFRTSIWDETLYKAWSSIVYOT.PPNVOOT.ER	NT.DN
FAEIIEADEVLLFERATFLVISHYOCKECRDAHRFEKISI	IIKO
FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVM:	DPSI
PSAATLINIRNARKHFEKLERVDGPKQCLLMR  6052 566 1718 KGLEPTCOMMESSAGEVTTEKENI GDDUNDAN GERSAGE	
	GWVL
PNTAMKKKVLLMGKSGSGKTSMRSIIFANYLARDTRRLGA	TILD
RIHSLQINSSLSTYSLVDSVGWTKTFDVEHSHVRFLONLV DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEI	TMTM
YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKERI	DMHY
RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEN	RDDK
FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISM	TTKO
PKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMS	DDST
PSAATLINIRNARKHPEKLERVDGPKQCLLMR	
6053 201 1704 KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRF	AGPA
HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFF	LLPG
HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFN	ASSM
LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSA	ASD
RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTI	CVFM
HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGC	ATLL
PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQAN TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFN	
GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEGYL	
MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEERGIL	
QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLG	1990
APGLIMAVGQDLYCYSYS	
6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNH	
KQSSSQQRKNFFFRRQRDISHSIVLPAAVSSAHPVPKHIK	VOGS
VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGK	
DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNN	SLKV
GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDE	/LCH
LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQV	JLCH JLCH JCKK
VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITE FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKL	LKV /LCH CGKK
PATABOON LANGUAGE TO A VOID A TOWN SAUFEST VELLE SEGRET TELE	LKV /LCH CGKK CPHF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	sequence	sequence	Codon, /=possible nucleotide deletion,
6055	421	2364	\=possible nucleotide insertion)
0055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLQCSALHHDP
1 1		l	GCANCSRFCRDCSPPACQCHTHVFPGNALNGVQPPELSRTLALI
i I			SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELQHGLAGICM
1 1		ľ	TLLITGDS IVSAEAVWDHVTWANRELAFKAGDVIKVLDASNKDW
			WWGQIDDEEGWFPASFVRLWVNHEDEVEBGPSDVQNGHLDPNSD CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKOC
1			RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQHFF
1 1			BACRLLQCMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH
1 1			SDYRYVAAALAVMRNVTQQINERERRLENIDKIAQWQASVLDWE
1 1			GEDILDRSSELIYIGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK
			KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFKLH
1			NKETBEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFEISE
1 1			NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP
1 1			\DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK
6056	43	3358	SGGRGPVRVRSEQLSFSAEQVSQISQISLGRRPLSSLPPPPSRA
			LAPTRAPDTALTIMEVAEVESPLNPSCKINTFRPSMEEFREFNK
			YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQO
			MVTGQSGLFTQYNIQKKAMTVKEFROLANSGKYCTPRYLDYEDL
1 1			ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE
1 3			EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEP
1 1			KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISPSV
1 1			LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT
1 1			VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD
1 1			IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP
1			KADEEBEVSDBVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA
1 1			SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA
1			YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS
1 1			SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS
1 1	i		IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI
1 1			REEVEETESWAXPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI
1 1			CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF
1 1			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
1 1			EICDGWLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMCA
1 1			VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA
1 1			CIQCSYGRCPASFHVTCAFAAGVL\MEPDDWPYVVNITCFRHKV
1			NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV
1			MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG
	1		AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF
1			VSAGRCHLGTCQVNSLSSFHVSQAQQETYLGFWINSKXSQCNIF
6057	1		LSGTY
005/	-	853	PVARLKEQEGEOGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ
1 1			GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS
1 1			RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG
1 1			WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS
1 1	1		ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR
1 1			TSLFTHDPAKICSRDHAQSSATWSCSQFFXVVCVYIAFYSTDYR
6058	1	986	LVQKVCPDYNYHSDTPYYPSG
0050	1	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
i I			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
	i	ļ	VLDACSSEATHVVMEETSAREAVSWQERRMAAAPPGCTPPALLD
1	1	J	ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
	1	J	PTPLTHHNTGLSEALETLAEAAGFEGSEGRLLTFCRAASVLKAL
1		J	PSFVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/
			RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP
6059	2	0.500	SREAGPWASLNCTLDPSASTP
0000	2	3650	QQDFESLADLTDHRAHRCPGDGDDDDPQLSWVASSFSSKDVASPT
1 1	l	1	QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH
		I	SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS
1	ı	- 1	
			RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK EHLAKSEKBAKKDDFMCDYCEDTFSQTEELEKHVLTRHPQLSEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F≈Phenylalanine, G-Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	sequence	Codon, /=possible nucleotide deletion, 
	Dequence		ADLQCIHCPEVFVDENFLAHIHQAHANQKHXCPMCPE\QFSSV
1			\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1	1	l	ERGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
	Į.		SDGNNAFFCNQCSMGFLT3SSLTEHIQ\Q\AHCSVGSAKLESPV
	i		VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
			KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNOCDLK
1			FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
ĺ			YMTTSTHYVCESCDKQPSSVDD\LQKH\LLDMPHPLCCTHCT\L
	I		CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
			VHVKHSHLGNPAKAHKCIFCGETFSTEVELQCHITTHSKKYNCK
1	J .		FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
1			PADLQGMLLKNPEAPNSHEASEDDVDASEPNYGCDICGAAYTME VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
			NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
			TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMOTVT
			STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
1			SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
1			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV
			PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM
			FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
6060	2145	202	VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
1 0000	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
1			DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
i			LTCHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
			GGI.PTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
į.			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLAV
i			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
			DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
1			SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
1			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVFGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
			QDRVIDGQDLLPLLLGTAQHSDHEFIMHYCERFLHAARWHQRDR
I	l		GTMWKVHFVTFVFQPEGAGACYGRKVCPCFGEKVVHHDPFLLFD
1 .	l l		LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHORTLSPVPLO
			LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
6061	110	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESBQGSPN
1			VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
			ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
			VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ
			SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
			RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRORTVLN
		Ì	PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
			LALHRRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
		J	LIVLFWGSKHFWPEVPKKAYDNEHTFYSNGEKKKIYMEIDPVTR
			TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
	1	j	EFSEPEEE DENEHITTTFFEQSVIWVPAEKPIENRDFLKNSKI
	1	ļ	LEICDNVTMYW\INPTL\ISGTFAKQLHHNPAFIILVSELQDFF
	l		EEGEDLHFPANEKKGIEONEOWVYPOVKVEKTRHARQASEEELP
	I		INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
			LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPUTR
	ĺ		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1 1	ļ	j	BFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
			LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSBLQDFE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EBGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
ì			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
6064	913	311	YPYCYQGGRVICRVIMPCNWWVARMLGRV NLPQSLPRPTEHSPPYSLEKMTDLVAUWDVALSDGVHKIEFEHG
	1	311	TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKATINID
			AISGFAYEYTLEINGKSLKKYMEDRSKTINTWVLHMDGENFRIV
			LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
			SSG\KRKEGIIHTLIVDNREIPEIAS
6065	1153	641	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAOGVAFILEDATG
			AEKEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
í I		ĺ	ELYAAARRVLGYDLLELSLHGPQETLDRTVHCOPAIFVASLAAV
			EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
			EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
1 1			VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
			QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
!!!			ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV
i			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV
			CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
			SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDISMLKT
			GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPROKPFOS
			GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT
i 1			HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK
			EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF
1			SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK
			QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
			NTWTPICNTREHCKGKSDHYWVVGIHENPQCLRCIPCKGSRFPP
			TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
1			KNGYEYBESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL
			MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE EEERDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
			KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS
i			SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
- 1			LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI
			CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM
			IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN
			QEBKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE
6067	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF
i			PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL
	1	ļ	GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV
- 1			SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP
6068	13	1730	
,,,,,		1/30	GSKMADLANEEKPATAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
	!	1	RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
	i		PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
- 1	1	ľ	FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
Į.			RSPSEAADEVCALEEKEPQKNESSNASEEKACEKKDPATQQAFV
1	ĺ		FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS
			SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA
- 1			AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT
		1	GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
	i		TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
- 1		i i	DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEGEAK
		1	MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGOTTGS
5050			T
6069	583	27	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
	1		RHARVTVKYDRRELQRRLDVEKWIDGRLESLYRGMEADMPDEIN IDELLELESBEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

	SEO	Predicted		
	ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	to first	H-Histidine, I-Isoleucine, K-Lysine,
	ł	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine,
		amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
	ĺ	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion.
		sequence	ocquence	\=possible nucleotide insertion)
		codeenco		Q\PGLRQFSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
	1			RPALLCVLSCI
	6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
			""	TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
				RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
	6071	2	1,654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
				VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
				ARLTLGRWERAPLASQGWKSRRAKRDHFSIERAQQEAPAVRKLS
				SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
				GRHVVCAAETGSGKTLSYLLPLLORLLG\HPSLDSLPIPAPRGL
				VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLOLS
				ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
				FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
			1	LLNKVASPDAVTTITSSKLHCIMPHVKOTFLRLKGADKVAELVH
			1	ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIOHLRL
				QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
			i	YDFPPTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
				ELAARRRSLPGLASSVKEPLPQAT
	6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
				VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDOLL
				VESCONEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
				VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
	1			AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
				CAKEITCQATIDKNVERMGRLLGLETNV
	6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
	6074	100		LVEATKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA
	00/4	168	1110	PGARCMATELCCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
				GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
	1			DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR DKTASRGDFMFSADRLIRLVVEEGLNOLPYKECHVTTPTGYKYE
				GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIOSDEET
				QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
				VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
				CKYFGTD
	6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
				KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
- 1		ĺ		LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
				NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
		l		VELCDHVHVYGMVPPNYCSORPRLQRMPYHYYEPKGPDECVTYI
				QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
	6076	1721	107	HPSPTEAPRVQHLTMDCTWRTLFLVAAATGTHAQVQLVQSGAEV
i				KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
				GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
				HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
				LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPSIQRRDSYYMTS
1	1	ļ		SQLSTPLQQWRQGEYKCVVQHTASKSKKE"FRWPESPKAQASSV
	J			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
	- 1	1		TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
1	Į			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
				GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
				A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ PSTTEWA\WGVLDVDABDEDODATVTGVVGUEDGETLINGGDG
		1		RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK
-	6077	3687	1268	LLPDMNLQP1FWIGLISSVCCVFAQTDENRCLKANAKSCGECTO
			1.00	AGPNCGWCTNSTFLOEGMPTSARCDDLEALKKKGCPPDDIENPR
				GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
1	-			QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
- 1	- 1			EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
- 1				PFSYKNVLSLTNKGEVFNELVGKORISGNLDSPEGGFDAIMOVA
Į.				VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLFNDGQCHL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	*	\=possible nucleotide insertion)
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTERFQPVYKE
			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
j.	ļ	ļ	GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
			CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
i			EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
1			FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
	1		NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC
1			NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
			FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
			VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
}	1		IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
6078	1425	180	KSAVTTVVNPKYEGK
0078	1425	180	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNPCKKCLEGILE GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
1	j		NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
	l		GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
			LAVMQAYDPEINKLNTILQEQRMAFNIABAFKDVSEPIVFLCOM
			QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
1			LSLPQDTGTFISKIPWSFYKLFLLILLIGLVIVFGPTMFLEWSL
			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
			RFKMFTLVVLNNVABFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
			GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
			LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
1			NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
i i			HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQFL
			LLDTPAQLWYFMLQYLQTAQSRGNDLVEILSFLFQLSFSTLGKD
			YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
			SSGVSGAGGTVHQPGFIV\VBTNYRLYAYTESELQIALIALFSE
1 .			MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
			VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF ELL\LAHAPKLGVLVFE/NTFAKRLMVVTPAGHSDVKRFWKROK
			HSS
6080	1	1199	TETIDHYGEFAMAAQAAGYSRQRAATQGLGSNQNALKYLGODFK
[			TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR
1			PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
1			YRVVPRDQDFQENYAGIFHFQPLCPPS?\FWOYGEWVEVVIDDR
	J		LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
1			EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
			SAABABAITSQKLVKSHAYSVTGVEEVNFQGHPEKLIRLRNPWG
			EVENSGAMSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR
1.			QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
			PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIPVHC
			SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
1 1			TQGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
			KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
			PPIPSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
			GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
6083	283	1288	ILSPEKKAVRAVEVBENVYAVMG
****	203	1500	EARSPGPTOTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD PESVGQPEEASPEEQPREASABEERPEDQQEKKAAAAA\Y\LDE
1 1	1		LPEPLLA/LRVLAALPRHE\LVOACR\LVCLRWKELVDGAPLWL
1			LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
1 1	1	ĺ	EGNCDVEHGGDGWRVEELFGDSGVEFTHDESVKKYFASSFEWCR
	i	J	KAQVIDLQABGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
1 1			KLLSHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
	I	ļ	FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309	KOWCAERRGLGMSLADELLADLEFAAEEEEGGSYGEEEEEPAIE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	D-Dedine, Made mionine, N-Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLNDSKMFAEIMMKIEEYISKQAKA
	ļ		SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
		l	FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1			VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
1	í	I	SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1			AORKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
			RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
	İ		QEPPPVKQVKPLFAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
1	1		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
1			RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
			VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6084	1865	309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPATE
1			DVQEETQLDLSGDSVETIAKLWDSKMFAEIMMKIEEYISKOAKA
1			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
1	1		FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1			VVSVTASTTQGQQLSEEELERLEEACDMALBLNASKHRIYEYVE
1			SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
	1		AQRKTLSGPSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	i		POWER TO SEE A PORT OF THE STITUTE O
i	1		RREAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
			QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
			ANRMS FGE IEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
			RISKTLORTIOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
			VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
			GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
1			DEEAYVLYHRAQTGAFCLSFDIVRDHLGDNRTELPLTLYLCAGT
			QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEEEDEEDEEER
1			KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALR
1			RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
			VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLOW
	l i		SPTENTVFASCSADASIRIWDIRAAPSKACHLTTATAHDGDVNV
1 1			ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT
1 1			CHEMIDODOCHER & CONDICOTROUPL C (THE PROPERTY OF THE PROPERTY
1 1			SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPBAGDVBADPG
1 1			LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
6086	2419		ISV
0000	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
			YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP
1 1			NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKIVVVLDSMIKV
1 1			PTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG
1			HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT
1		i	LIRIFDTSSGHLIQELRRGSOAANIYCINFNODASLICVSSDHG
1 1		1	TVHIFAARDPKRNKQSSLASASFLPKYFSSKWSFSKPQVPSGSP
1 1			CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
			DDKL
6087	476	1877	QNSQRTGLPITIFSRSPPLLTGSDLCHNMPCTCTWRNWROWIRP
1 1			LVAVIYLVSIVVAVPLCVWELQKLEVGIHTKAWFIAGIFLLLTI
1 1	1	J	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
1	[	J	CIATUUDECHIOOPANII TOPELQUPI I KILWWVPI ISLDSWIALKYP
1			GIAIYVDTCRECYBAYVIYNFMGFLTNYLTNRYPKLVLILEAKD
1			QQKHPPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
			CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
	l		EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
1	l	1	EWQTVEAVATGLODFIICIEMFLAAIA\HHYTFSYKPYVQEABE
1 1	I		GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
1			DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
1			TTAKISDETLSDTIGEKKEPSDKSVDS
5088	1684	689	GASGLVRIAQOGHRCLLAPVAPKLVPPVRGVKKGFRAAPRPQKE
			LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDI,L
1 1	J		KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNOELSEGGTSF
1 1			
1		1	SOTCLTOFLEDEYPOMPTEGIKNLVDFLTGEEVVCHVARNLAVE
[ ]		- 1	QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
$\overline{}$			TOWTGKELFEMWKIINPMGLLVBELKKRNVSAPESRLTRQSG\A

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	Gidcamic Acid, Farhenyidianine, GaGlycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
!	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
-	sequence		\=possible nucleotide insertion)
1			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
			TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHPLCHSWTGSRAGAHTGAPAW
			PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLOK
1		i	LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
	I		PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
			QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
1			LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
1	1		VSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLOKDD
1	1	Ī	KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTODHLPRVVVVG
	1		DQSAGKTSVLEMIAQARIFPRGSGEMWTRSPVKVTLSEGPHHVA
	Į.		LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
			LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
1			DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
1			AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
			REYEEFFONSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES
ļ			VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
1		!	EVISLSQVTPKHWEEILCQSLWERVSTHVIENIYLPAACTMNSG
		ĺ	TFNTTVDIKLKOWTDKOLPNKAVEVAWETLOEEFSRFMTEPKGK
	1		EHDDIFDKLKEAVKERSIKRHKWNDFAEDSLRVIQHNALEDRSI
1		ł	SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
			KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
			CDCVIEWDDGI TENDENHOUNDRING WEST AND CONTROL OF THE
1		ļ	SRGVEVDPSL_KDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
	!		FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
			KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE ALHQEK
6090	194	1560	
0000	134	1500	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL
1			FELQLPFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
			FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
			FNLLMYTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAABLR
			FNLLMYTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTLR\RRGSSTODS
	-		FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV LTATGMSLCRSLHHERTTSFLNIL/FPLLSVMDVHSVPAAELR P\RTTSLFNHNASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNNRMKEVLVSSML
	-		FNLIMVTTIVUGRRFIGSIVKEASCRKWSLERSILLPLTRETV LTATGMSLCPSLHLERTVSELNLL/PLLSVMDVHSVPAAELR P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTLR\RRSSSTODS CMARTDCS/PHACCLSPSLIRSBUSTLKMDFNMEMKEVLVSSML SAYTVAFPWVFVKYNTYTYDKRMSCELFLUVSISTSVILMCHLL
			FNILMYTTIVLGRAFIGSIVKEASORGKYSLFSSILLFLIFITY LITATONSLOSSILHIFFTYSENILL/FPOLISVODHSVARAEL FVRKTSLENHMASKOPBEAVSGLAKSEDYLLTIR.RESISTODS CHARTDCF/SHCCLSSSILRSEWETLMOPMENKEXUVSSML SATYVAFFFWEVKNTHYYDRHSCSLFLLVSISTSVILMOHLI SATYVAFFFWEVKNTHYYDRHSCSLFLLVSISTSVILMOHLI PASYCDLIHRAABHLGGWCWDPALCSWIZJHWYEBCWMPGDV
	-		FINLINYTITUGERFIGSIYKERSORGKVSLEPSILLELTEFTY LIATIONSLEPSILLEPTYS FENLLY FPELSIVOVYSISVABLE; P\RKTSLFMHASHGPBRAVSGLAKSRDYLLTLE\RRSSTQDS CMARTPCP/PHACCLSPSLISSEVERLOMOFNEMERKYLSSML SAYTVAFVVAFVXHTYTYDKRNSCELFLUVSISTSVILMGHLE PASYGDLHKRAAHLGCMCKVDFALCSNVLQFFFTSECMPGOV LVKHSKRVYKVAKOHYNVALDSUSFEPFFFFSSPLFLIKILLILL
	-		FILLIMYTTIVLGREFIGSIVERSORGKVSLEPSILLEFITEFTY LTATGNSLOSSILLEFRTYSELMIL/PFILLSFUNDYSARELR PLATTSILSFRIMMASKOPRANGCLANSEDVLLTLEVERSSSTODS OARSTOC/FIRLCLSSELTSSEVETLDDONNEWSLVVSSML SAYTVAFFVWWFVXFHTYDTRMSCELFLUSSISTSVILMGHLI PASYCOLLHRAAMLCCKOVLDFUNSTSSVILMGHLI LUKHSKNYYKAVGHYMVALDSDVSHFPFFFFFSKLFRIMTLLI LEGAVIVYGVILMSSERHMGTSLALLILFSNYVAFKLEDBEL LEGAVIVYGVILMSSERHMGTSLALLILFSNYVAFKLEDBEL
5003			FILLIMYTTIVLGRSFIGSIVERSGCRGVSLFPSILLFITEFTY LTATGNSLCSSLLHERTYSFELLIFPSILFSLTSLFPSILLFITEFTY PRETISENMENASGGERGANGCLANSEDVLLTLRVERGSSFTODS OARTHOOF PRETICLEDSLIESSEPTIMODPONNERSULVISSEL PRETISENMENASGGERGANGCLANSEDVLLTLRVENSSSTSVILMGHLU PRETICLEDSLIESSEPTIMODPONNERSULVISSEL PRETICLEDSLIESSEPTIMODPONNERSULVISSEL PRETICLEDSLIESSEPTIMODPONNERSULVISSEL PRETICLEDSLIESSEPTIMODPONNERSULVISSEL LEGANIVALISSEPTIMOTISLALILESNIVAFFKLLEDRL UGGANIVAGNODDLERES
6091	3279	412	FILLIMYTTIVLGREFIGSIVERSORGKVSLPSSILLEFITEFIT LIATGNSILCSBILLEFRITSELLILFPELSVERDVSARELE PLRITEISLPHEMASKOPRANGCLANSEDVLLTLEVREGSSTODS OARTHCOF/HUCCLSBILLSBEVERDUDDNEMBEVLVNSMIL SAYTVAFPVMFVLVNTHYDRANGCEPFLUSSISTSVILMGHLI SAYTVAFPVMFVLVNTHYDRANGCEPFLUSSISTSVILMGHLI PASYCOLLHARAALICCK(NVDHOELGSNIVLDHWTSECMPGOV ULKHSKNYYKAVGHYMVALDSDVSHFPPFFFFSKULRILINLL LEGAVLYVQU/SULASSERMIGHTSLALLILFSNYAFFKLLEDKL VLSKAYSYSASDORDLERES SSKYREMBERSELERGKELLGGULDDYKTLNGKASPGTDASG
6091	3279	412	FILLIMYTTIVLGRFFGGSTVERSGCRKVSLFPSILLFITEFTY LTATGSSLCSSLLTHETYTSFELLIFPSILSFELLFFSSLTLTSFSLTSFSSTCDS PARTICSFSTCDSSTCDSSLTSFSSLTSFSSTCDSSTCDSSTCDSSTCDSSTCDSSTCDSSTCDSS
6091	3279	412	FILLIMYTTIVLGRZPIGSIVERSCRGKVSLPSSILLETTEFTY LTATGNSLCSSILLETTYSFELLITETTSELLTTETS PRETISENSHMASHGOPRAVGCLAKSEDVLLTLEVERSSSTODS OARTHCO/FIRCLSSELTSSILLETSSILLTENSHMASHGOPRAVGCLAKSEDVLLTLEVERSSSTODS SAYTVAFPVWFVLOTHYTDKMSCELFLUNSISTSVILMGHLIL SAYTVAFPVWFVLOTHYTDKMSCELFLUNSISTSVILMGHLIL LEGAVLTVOLVSLUMSSELMHGOTSLALLILFSNIVAFFKLLEDRL VLGKAVSTSASDOEDLERES SSKTEMBERSELTELGESLELGLEDDYTTLIGGARAFGTPAXS WOPPTHAGGARFARAYTERSPRGCTSSHHOGENKKYSLUMREPG SEPPPADAGARFULGRAGGOPPUTS
6091	3279	412	FILLIMYTTIVLGRFFGGSTVERSGCRKVSLFPSILLFITETTY LITATGNSLCSSLLHERTYSFELLI/FPLLSVGNFVSARELR PLRTISLSNRMANSKOPRANGGLANSDDYLLTLRLRSSSTODS OARTHCOS/INCLCLSPSLISSSYCTLMODPENERGUVUSSML SATYVAFVUMWEVLOTHIYDTRWSCERFLUNSSTSTVILMGHLIL PASTCULARIOANLCHCKVENDERSSTLMODPENERGUNSGENFORM LYGISSMYTANGHTWAT DODVSTIPFIFFFSKURELINILLIL LYGISSMYTANGHTWAT DODVSTIPFIFFFSKURELINILLIL LYGIASTYNANGHTWAT DODVSTIPFIFFSKURELINILLIL LYGIASTYNANGHTWAT DODVSTIPFIFFSKURELINILLIL LYGIASTYNANGHTWAT DODVSTIPFIFFSKURELINILLIL VICKARYSTNANGHTWAT DODVSTIPFIFFSKURELINILLIL VICKARYSTNANGHTWAT PROFITENSIANSTRANGHTWAT PROFITENSIANSTRANGHTWAT VROFTTYNGTARANTEPBRBGFGSSTHOPMONEXGUNDFOR PSDEPADRANGHTWAT VROFTTYNGTARANTEPBRBGFGSTHOPMONEXGUNDFOR PSDEPADRANGHTWAT VROFTTYNGTARANTEPBRBGFGTTWATORFGRGFTTWATORFGRGFTPROFTTYNGTARANTEPBRBGFGTPROFTTYNGTARANTEPBRBGFGTPROFTTYNGTARANTEPHRANGHTWAT VROFTTYNGTARANTEPBRBGFGTTWATORFGRGFTTWATORFGRGFTPROFTTYNGTARANTEPHRANGHTWAT VROFTTYNGTARANTEPBRBGFGTTWATORFGRGFTPROFTTYNGTARANTEPHRANGHTWATORFGRGFTPROFTTYNGTARANTEPHRANGHTWATORFGTTYNGTARANTEPHRANGHTWATORFGTTYNGTARANTEPHRANGHTWATORFGTTYNGTARANTEPHRANGHTWATORFGTTYNGTARANTEPHRANGHTWATORFGTTYNGTARANTENGTYNGTTYNGTARANTENGTYNGTYNGTARANTENGTYNGTARANTENGTYNGTARANTENGTYNGTARANTENGTYNGTARANTENGTYNGTYNGTYNGTYNGTYNGTYNGTYNGTYNGTYNGTY
6091	3279	412	FILLIAVTITULGREFIGS LYKEAGCRKYNSLEPSILLETLEFTUR FULLTURGREFIGS LYKEAGCRKYNSLEPSILLETLEFTUR FULLTYPILLSVANDYNARELR UNGTHENSWENDELITER VERSISTODS AND AND AND AND AND AND AND AND AND AND
6092	3279	412	FILLIMYTTIVLGRFFGGSTVERSCRKVSLFPSILLFITETTY LTATGNSLCSSLLTHETTYSFLML/FPLLSVGMVPVARAELE PLATGNSLCSSLLTHETTYSFLML/FPLLSVGMVPVARAELE PLATGNSLCSSLLTHETTYSFLML/FPLLSVGMVPVARAELE PLATGLSRMMVANGUPRAVOGLANSEDVLLTLTLRVRSSSTODS SANTYDAYPUWFVLOTHTYDRWSCEDFLUSSSTSTSVILMGHLI SAYTVAPFUWFVLOTHTYDRWSCEDFLUSSSTSTSVILMGHLI LTVASISKUVTANGHTWALIGENOSHTPPHFFFSRCLERINGLDL LTVASISKUVTANGHTWALIGENOSHTPPHFFFSRCLERINGLDL SARTEDBERGET LERGERLJGGLIDDYKTLIGGARAGTDA, AGS SARTEDBERGET LERGERLJGGLIDDYKTLIGGARAGTDA, AGS WOPPTTHSGDTARAEVPPRPBRGVSSHGOPBOKTACHNOP DE SBDPPDARAFELIGARAGOPPVQOVLUSGROPPGG VRPSTSGSSLASSGQAGSLEETTTHSGDGPRGAGSPPGG LOPSPTTARGTCSVSDDLINGVKRFKFFRVYSVGSVGSPRE BRYTYSSSLASSAGGAGSLEETTTHSGDGPRGAGSPPGG LOPSPTTARGTCSVSDDLINGVKRFKFFRVYSVGSVGSPRE
6091	3279	412	FILLIAVTITULGREFIGS IVERAGCROKUSELPSILLETITETY LITATUSALCESSILLETETYS ELLIPTISELT. PPILLSTANDYSPARAELR VARTISELSHAMMANGGRERAVGILATSEDTLITLE VERSSSTODS ANATYCE / PIRCLESSILESSETTLIMOTORMEGENE VUSSMIL PAST COLLATERABLICECOCONTORALCESTILESSET SUNSMIT PAST COLLATERABLICECOCONTORALCESTILESSET SUNSMIT PAST COLLATERABLICECOCONTORALCESTILESSET SUNSMIT PAST COLLATERABLICECOCONTORALCESTILESSET SUNSMIT PAST COLLATERABLICECOCONTORALCESTILESSET SUNSMIT PAST COLLATERABLICECOCONTORALCESTILESSET SUNSMIT PAST COLLATERABLICECTIC SUNSMIT PAST COLLATERABLICECTIC SUNSMIT PAST COLLATERABLICECTIC SUNSMIT PAST COLLATERABLICECTIC SUNSMIT PAST COLLATERABLICECTIC SUNSMIT PAST COLLATERABLICECTIC SUNSMIT PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLICE PAST COLLATERABLIC PA
6091	3279	412	FILLIMYTTITUCRSPIGSITYERSQCRKYSLPSILLETITETY LITATIONISCUSSILLETRYTSFELLITYPSILATOPIAGE PLATTISLENBINASHOPRANGILAISEDVILLTEN REGISTODS OARRICOS/INCLCESPILESESVETIMODENNERSULVISSBIL SAYTVAPOPURVUSHTYDENSCERFILMYSISTSVILMGHLIS SAYTVAPOPURVUSHTYDENSCERFILMYSISTSVILMGHLIS SAYTVAPOPURVUSHTYDENSCERFILMYSISTSVILMGHLIS SAYTVAPOPURVUSHTYDENSCERFILMYSISTSVILMGHLIS SAYTVANGHYNAVALDENVSHTYPIFFFSKEFERIMILLIS LOWALTYOLISLASSEKHAPTISLASSILMILSENNYAPTKLEDORI SARTISLASSINTANGHYNAVALDENVSHTYPIFFFSKEFERIMILLIS SARTISLASSINTANGHYNAVALDENVSHTYPIFFSKEFERIMILLIS SARTISLASSINTANGHYNAVALDENVSHTYPIFFSKEFERIMILLIS SARTISLASSINTANGHYNAVALDENVSHTYPIFFSKEFERIMILLISTANGHYNAVALDENVSHTYPIFFSKEFERIMILLISTANGHYNAVALDENVSHTYPIFFSKEFERIMILLISTANGHYNAVALDENVSHTYPIFFSKEFERIMINISTANGHYNAVALDENVSHTYPIFFSKEFERIMINISTANGHYNAVALDENVSHTYPIFFSKEFERIMINISTANGHYNAVALDENVSHTYPIFFSKEFERIMINISTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYPIFFARMYSVORYDDENS SARTISLASSINTANGHYNAVALDENVSHTYNAVALDENVSHTYNAMYSVORYDDENS SARTISLASSINTANGH
6091	3279	412	FILLIAVITITULGREFIGS IVERAGCROKUSLPSILLETITETY LITATUSSILCES LIHLEPRIYS ELILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALIDITUS VALID
6091	3279	412	FILLIMYTTIVLGREFIGS IVERSORGKVSLFPSILLETIFFTY LITATIONSLOSS INLEPRITYSELNLIPPILLSFULLPPILSFUL
6091	3279	412	FILLIAVITITULGREFIGS IVERAGCROKUSLPSILLETITETY LITATUSSILCES LIHLEPRIYS ELILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALILIPPILES VALIDITUS VALID
6092	3279	412	FILLIAWTTITUCRSFIGS IVERAGCROKUSTEPSILLETITETY LITATORSICOSILLETRITETELLIAPILETITETY LITATORSICOSILLETRITETELLIAPILETITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETY PASTCOLLHERARMICOCKOVERALCISTICOSIPPESCAMBOQUI PASTCOLLHERARMICOCKOVERALCISTICOSIPPESCAMBOQUI VERSINNYAFORGUSTAVA I DESIGNATORITETISTICASI SIRRIPETRITETISTICASILLETRITETISTICASICOSI SIRRIPETRITETISTICASILLETRITETISTICASICOSI SIRRIPETRICOSI DALITETISTICASICOSI SIRRIPETRITETISTICASI VERPETRICOSI DALITETISTICASICOSI SIRRIPETRITETISTICASI VERPETRICOSI DALITETISTICASI SIRRIPETRITETISTICASI VERPETRICOSI SIRRIPETRITETISTICASI SIRRIPETRICOSI SIRRIPETRIC
6091	3275	412	FILLIAWTTITUCRSFIGS IVERAGCROKUSTEPSILLETITETY LITATORSICOSILLETRITETELLIAPILETITETY LITATORSICOSILLETRITETELLIAPILETITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETULPPLASTICOSILLETRITETY PASTCOLLHERARMICOCKOVERALCISTICOSIPPESCAMBOQUI PASTCOLLHERARMICOCKOVERALCISTICOSIPPESCAMBOQUI VERSINNYAFORGUSTAVA I DESIGNATORITETISTICASI SIRRIPETRITETISTICASILLETRITETISTICASICOSI SIRRIPETRITETISTICASILLETRITETISTICASICOSI SIRRIPETRICOSI DALITETISTICASICOSI SIRRIPETRITETISTICASI VERPETRICOSI DALITETISTICASICOSI SIRRIPETRITETISTICASI VERPETRICOSI DALITETISTICASI SIRRIPETRITETISTICASI VERPETRICOSI SIRRIPETRITETISTICASI SIRRIPETRICOSI SIRRIPETRIC
6092	3275	412	FILLIAWTTITUCRSFIGSITWERSCROKUSTPSILLETITETY LITATISMISLOSILLIPETYSFELLI/PPLISAWIDVSPARAELE PLATISSISLOSILLIPETYSFELLI/PPLISAWIDVSPARAELE PLATISSISLOSILLIPETYSFELLI/PPLISAWIDVSPARAELE PLATISSIPMIMASIGGEREAUSCLAISEDVILLIPETASSISTODS SANTICA/PPURPAVILLIPETASSISCOSILIPETASSISTONIAGHLI SANTIVA/PPURPAVILLIPETASSISCOSILIPETASSISTONIAGHLI LUGARATYSPARAELEPETASSISTONIAGHLI LUGARSTYSASSISONIAGHLIPETYSFERSETETATILLI LUGARSTYSASSISTONIAGHLIPETYSFERSETETATILLI LUGARSTYSASSISTONIAGHLIPETYSFERSETETATILLI LUGARSTYSASSISTONIAGHLIPETYSFERSETETATILLI LUGARSTYSASSISTONIAGHLIPETYSFERSETETATILLI LUGARSTYSASSISTONIAGHLIPETYSFERSETETASSISTONIAGHLIPETYS PROPRIESENSISTONIAGHLIPETYSFERSETETASSISTONIAGHLIPETYSFERSETETASSISTONIAGHLIPETYSTONIAGHLIPE
6091	3275	412	FILLIAWTTITUCHERFIGS IVERAGCREKVSI-PSILLIFITETTU LITATUSALCESILIHERTYS FELLI-PFILESUNDYSPARAELE VARTISIAWHENASIGDERAVISCLAISEDILLITA LREASISTODE ANATTETY PIECULSISSILISESYTEMODENWENGUVUSBIL PASTCOLLHENASIGDERAVISCLAISEDILLITA LREASISTODE PASTCOLLHENASIGOROGUNDERACISHICIPSTESICARDOOV LIVESISHIVIYAKONGUNTAVIA DEDVICTIONETSICARDOOV LIVESISHIVIYAKONGUNTAVIA DEDVICTIONETSICARDOOV LIVESISHIVIYAKONGUNTAVIA DEDVICTIONETSICARDOOV LUKARISTANDA PARATIFEDERSCOSSHOOPETSICARDOOV MOPPTHIGABRA PARATIFEDERSCOSSHOOPETSICARDOOV MOPPTHIGABRA PARATIFEDERSCOSSHOOPETSICARDOOV MOPPTHIGABRA LIVEDERSCOSSHOOPETSICARDOOV MOPPTHIGABRA VITEDERSCOSSHOOPETSICARDOOV MOPPTHIGAB
6092	3279	412	FILLIMYTTITUCRSPIGSITYERSQRGKYSLPSILLETITETY LITATGSSILDSILLHERTYSFELLI/PPLISANDYPSARELE PLATGSSILDSILLHERTYSFELLI/PPLISANDYPSARELE PLATGSSILDSILLHERTYSFELLI/PPLISANDYPSARELE PLATGSSILGSILLHERTYSFELLI/PPLISANDYPSARELE PLATGSILGSILLHERTYSFELLI/PPLISANDYPSARELE SATTUA/PUWWINGLESSILGSILDSILGSILGSILGSILGSILGSILGSILGSILGSILDSILGSILGSILGSILGSILGSILGSILGSILGSILGSILG
6091	3275	412	FILLIAWTTIVLGR.FIGS.IVERASCRKVSI.FPSILLET.TEFTY LITATIONSLOSS.IULTERTYS ELILI.FPILLSTRUMPYSABELE PARTISLENBIMASIGGERAVGICLASS.BOTLLIT.R. PRESSSTODS OAMTICE/PILCLESS.LITSEYSTLOMORMERSULVISBIL PASTCOLLHUANASIGGERAVGICLASS.BOTLLIT.R. PRESSSTODS PASTCOLLHUANASIGGERAVGICLASS.BOTLLIT.R. PRESSSTODS PASTCOLLHUANASIGGERAVGICLASS.BOTLLIT.R. PRESSSTODS PASTCOLLHUANASIGGERAVGICLASS.BOTLLIT.R. PRESSSTORE PRESSTORE P
6092	3279	412	FILLIAWTTITUCRSFIGSITVERASCREVISTESILLETITETTU LITATENSILCESILLETITETTU IPPLISTATUTU PPULSTAVOHVARAELE LITATENSILCESILLETITETSILTIPTI IPPLISTAVOHVARAELE LITATENSILORIAMINASCRERAVISCIAUSEDVILLTIA (RESISSICODE ANTANAFVENIVOLINIAMINASCRETALISEDVILLTIA (RESISSICODE ASTYVANIVOLINIAMINASCRETALISEDVILLTIA (RESISSICODE ASTYVANIVOLINIAMINASCRETALISEDVILLETIA (RESISSICODE ASTYVANIVOLINIAMINASCRETALISEDVILLETIA (RESISSICODE) ASSICTATION ORGANICATION ORGA
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1 KD 5094 23 1010 PFIRCLIKRDQNAEMSERKVLIKKYYPDDSDSKIPKINLIPKDROY VVELKAAPPRINCKYTCOSYTYNGKRYNARKETVQNOVIJGLPFR FYTKCTRCLARIFTRYTDBFINDTVITEHGATTPRIQAKLILAESKER RVQKRREDSELIMPRIVLANTYTOSKILAESKER RVQKRREDSELIMPRIVLANTYTOSKILAESKERALISEKKOLKOR QNAVDPRANDAGRIKISESSERGOQOETDOSGTAALIERAKKRIL LEDDSDDDBAAPSFILQPALRIPPTATIODAFKYRKVINGSV QOPYTDDNAVIJERTOTICTD QOPYTDDNAVIJERTOTICTD GOPYTDNAVIJERTOTICTD GOPYTDNAVIJERTOTICTD GOPYTDNAVIJERTOTICTD SOSSENGWARMASHVOQDODOLD GORGREGAKYVKYNONOCOCOP YTTICKPLOPOSKIKKVLKKMLKFILAKGEVYKSSCK DSPMD STMODAVAGRALIKKKULOGUKTLAGISKESSGKNIKKS	1		}	
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PYLICTECLASITE TYTOPENTO TYTHERIGATEN FOARKLISEERK RVOKERGEESELIMPHIVKLUSHT FUCK MELKEVELOGELISEERKOK OAHUP FRANLESERSKEN FUCK KLEWELOGELISEERKOK OAHUP FRANLESERSREN OGEEDSGETAALLEERKREL LEISIGS BEGERAPHS, FOARKEN FUCK ALLEES OGES GERAPESER FOARKEN FUCK FUCK FUCK FUCK FUCK FUCK FUCK FUCK	6094	23	1010	
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EPQELLQSQDFVGEKLGSGEPSHS				EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M-Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		į .	VKVHTVPKPGKGADLSKPPCRKAKEIRKBRKRLKLMQQNPAGEL
1			EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR
			VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR
			FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN
1	i	1	CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY
1			MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK
			YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS EBAAVLQYASLVGQKCSERMLLFRN
6096	2277	575	QRVRAALLSSAMEDSEALGFEHNGLDPRILQAVTDLGWSRPTLI
		315	QEKAI PLALEGKOLLARARTGSGKTAAYAI PMLQLLLHRKATGP
			VVEQAVRGLVLVPTKELARQAQSNIQQLATYCARDVRVANVSAA
			EDSVSQRAVLMEKPDVVVGTPSRILSHLCQDSLKLRDSLELLVV
i i		1	DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQALKE
			LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK
			LSLIRGKSLLPVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSR
1			CHITSQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKCDKASDP
	İ		EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV
			LTFVLPTEQFHLGKIEELLSGENRGPILLPYQFRMEEIEGFRYR
1	1		CRDAMRSVTKQAIREARLKEIKEBLLHSEKLKTYFEDNPR\DLO
i			LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL
			PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS
6097	1673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPOPPTGPP
			PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP
			YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL
			ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ
1			LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSL
			RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDS
			RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL
			DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLLRALA\SPEOLGSAGPPRGVPR\LGPPA
			PNGPPVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG
			VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET
1			QPPPSLPGTPOO
6098	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
			EGKIPKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
1			RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
			NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
1 1			\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
			TAMEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
			ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6099	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
			EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
1			RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
	J		NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
1			\OFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
1 1	1	i	TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
6100	2	733	ELTKEKDQIEAALSRMPSPGGRITLQTRLMQEAFGRSFGKD
0.100	<u> </u>	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL
1			QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
		J	RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM
1			VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN
]			VERAFINTAKEIYRKIQQGLPDVHNEANGIKIGPQQSISTSVGP
6101	1	1399	SASQRNSRDIGSNSGCC
	*	1399	PRGRAWPLREVSHWIGGERVCSWSASWGRLPALSARLSPLLAFR GRMVEPLSCAVOOVANGENCENCENCENTERING
1		i	GKNVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF
			AMERICAN RODALI DOMESTA POR LINGUIS ROLL TO THE PROPERTY OF TH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			NGNLPFLPKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
		ł	KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
l .	J.	l	LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1			QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
1			MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
1			G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
i i	i		FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	OTPOATLAANGAEDSRGGENLPAGEIGASPAAPCCSESGDERKN
			LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
	ŀ		SLKKLDKLIEGRTVSKMQLEEGVLTISSEIPKRIRSALKNAEES
J			KQFLNQFLEQETHLFSAINSHLLTAQFWNDDLGTMISQIEEIER
			HLAYLKWISQIEELSDNIQQYLMTWXVPEAASTLVSMAELDIKL
	1		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
			PPQSQTVGLSRPASAPRIYSYLETLPCQLLKLQTSHELLTEPK\
		1	HSQKNTLFLPPLLSS/WPIQVNLTPLOKRFRYHFRGNROTNVLS
1			KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
ł			LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
			GTFASCMHILSEETCFQRWLTVERKFALOKNDSMLSSEAAWVSO
			YKDITOVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE
1			LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
1			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
i			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
1			AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
1 .			VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
6103	207	2523	KHIKBACIVLNUNVGSALTAGKDVLPVQLQGSFPAT ESNSTMTTYLEFIQQNEERDGVRFSNNVWPSSRLEATRMVVPVA
0200	207	4323	
1			ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
1			PLIFLYVVDTCMEDEDLQALKESNQMSLSLLPPTALVGLITFGR
			MVQVHELGCEGISKSYVFRGTKDLSAKQLQENLGLSKVPVTQAT
			RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
1			PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
			DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
1			YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
i I			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
			ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNOHNAPIFOGG\RG
			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
1			QEAAAILMARLAIYRAETEEGPDVLRWLDRCLIRLCQKFGEYHK
			DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
1			DTFPQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
1			ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGOES
1			GAPILTDDVSLQVFMDHLKKLAVSSAA
6104	124	732	KVSEYIILSKUKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
"			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
1			LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
	J		LKOKHVLCAYCYEKVCKETAEIRROIGKOEGGPPKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTON
6105	3	989	PLHGACTSLVLORFCHRRPRPCAPARPEDMRRPAAVPLLLLCF
	۱ ۲	,00	GSQRAKAATACGRPRMLNRMVGGQDTQEGENPWQVSIQRNGSHF
1 1			CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM
1 1			YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
1 1		1	
	1	J	PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR CNLLYSKDTEFGYOPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
1	1		
			CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK

Deginning nucleotide location corresponding to first amino acid sa	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
Docation   Cocation   Cocation   Cocation   Corresponding   Cofficient   Cofficie				/A-Dississ C. Containing Signal peptide
Location   Corresponding   Coffee   C				
to first amino acid for first man can can control for the first man can can can can can can can can can c	110.			Giucamic Acid, F=Fnenylalanine, G=Glycine,
to first amino acid am				
amino acid residue of render of residue of residue of amino acid adjusted equence control of the	1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence (Codon, 'Apossible mucleotide delation) sequence (Codon, 'Apossible mucleotide delation) (Codon	1			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /-possible mucleotide deletion. 1000 Sequence Codon, /-possible mucleotide insertion) 1000 Sequence Cooperation but of the insertion in the control of the cont	1			S=Serine, T=Threonine, V=Valine,
Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6106 3 1302 GRPPFAIRIDERPTAINSOPELOLEXGCAELLTSTUSRGEPAN AGLARDRICALAMMULRARAPHANATRERAGSPRACAPREPACTOR AGLARDRICALAMMULRARAPHANATRERAGSPRACAPREPACTOR AGLARDRICALAMMULRARAPHANATRERAGSPRACAPREPACTOR LIXTELESKEECCSTORISTSTEEDVALITHTENHITHOGRAPH GENERAL CONTROLLARACTOR DELIVOYOGGAEVATORIO ULXTELESKEECCSTORISTSTEEDVALITHTENHITHOGRAPH GENERAL CONTROLLARACTORIOEBRACAPREVALTORIOEBRACAPRE BUDOKTYTHOLALIARACTORIOEBRACAPREVALTORIOEBRACAPREVALTORIO GENERAL CONTROLLARACTORIOEBRACAPREVALTORI	1		sequence	Codon, /=possible nucleotide deletion,
S196   S		sequence		\=possible nucleotide inscrtion)
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6107 623 168 SINGSSPREPERKORGKY, LASPBERKEWTEPTACDERHOYJLES DEPKTAYMULGYPROKIEUTOSHISINENSTIGITESPILITYKK KERAGYPAREVIRI FETAFOTYYRGGULLEDPKIAFRQUARUE KERAGYPAREVIRI FETAFOTYYRGGULLEDPKIAFRQUARUE KERAGYPAREVIRI FETAFOTYYRGGULLEDPKIAFRQUARUE KERAGYPAREVIRI FETAFOTYYRGGULLEDPKIAFRQUARUE GESTAFOTY LENGTH FOR THE TOTYTH FOR THE TOTYTH COSMITLE LAPTIPHISTE DAWN LILLAR FOR THE TOTYTH COSMITLE KERAGYPAREVIRI FETAFOTY HAN THE TOTYTH COSMITLE LAPTIPHIST DAYNHER DAWN LILLAR FYTAKUS THE TOTYTH FETAFOTY HAN THE TOTYTH FOR THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH FETAFOTH THE TOTYTH THE TOTYTH FETAFOTH THE TOTYTH THE TOTT THE TOTYTH THE TOTYTH THE TOTYTH THE TOTYTH THE TOTYTH THE TOTT THE TOTYTH THE TOTT THE TOTYTH THE TOTT THE TOTYTH THE TOTT THE TOTYTH THE TOTT THE TOTYTH THE TOTT THE TOTYTH THE TOTT THE TOTT TH	1			
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1	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
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			PGLRDFIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPPR
i			FGERDFIFWWQVQRWGVALSGEPVFFCWTECFYGFTAGNAFPFR   KPONTHRSW
6114	818	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
-	1 040	240	PISRPRPS/GSPANSWSACVSAAPSSSWPASSSWPCGPRRCCTR
			RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEQVQC
1			GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSOVT
1			GRPOWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
1	1	12	SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKBEEDESYTPVO
1		1430	AARPQTLNRPGQBLFRQLFRQLRYHESSGPLETLSRLRELCRWW
1			LRPDVLSKAQILELLVLEQFLSILFGELRVWVQLHNPESGEE/L
			WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAOLWSL
			ASPLRSSSALGDHLEPPYEIEARDFLAGOSDTPAAOMPALFFRE
			GCPGDQVTPTRSLTAQLQETMTFKDVEVTPSQDEWGWLDSAQRN
	1		LYRDVMLENYRNMASLGK
€117	1433	222	VGVPSPAPPCSWBVGPGGGWTPGILKEGQGGRRTPLLLLATRTR
			GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA
1			SMDFADLPALFGATLSOEGLOGFLVEAHPDNACSPIAPPPPAPV
			NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM
1			VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN
1			TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK
1			\EQLKQI\PTHDYOKGDQYDVCAICLDEYBDGDKLRVLPCAHAV
1			HSRCVDPWLTQTRKTCFICKQPVHRGPGDEDQEEETQGQEEGDE
1			GEPROHPASERTPLLGSSPTL PTSFCSLAPAPLVFPGPSTDPPL
1			SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGNERGKVKK
1			KEKEKETQKEKIGEKGRE3KVKRKEVEQKIKQEKQEKQERRKGK
			EKEEKRTKOGKETNKEKROFKGOEEKGENKDSTLTPTTDI.RDI.RDI
1			EKEEKRTKQGKETWKEKEQFKGQEEKGENKDSTLTRTPLEPLEK
			EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQLLVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
			EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYNEMYLSN/ADSLARSFSVGFKQDSQP
			EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQLLVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
6119	1217	462	EKEEKRTKQGKETINEKKQPKGQEEKGENKDSTLTETPLEPLEK NKQILVLGLADAGKTSVLHALIASNPYQUELAVPTQGEHAVCINTE DSQMEFLRIGGSKPFRSYMEMYLSH/ADSLARSFSVGFKQDSQP ITMKAKKYLHQLIAANPYLPLVVTANKQDLEAAYHITDIHEALA II
6119	1217	462	EKEBERTKÖGKEINBERKOPKOGERKORKOSTI.TRTPLEPLEK KNÖLLVIGILOGAGKESVILISI.ASINVÖJGVAPPOÖJHAVCINTE DSQMEPLEIGGSKOPRSYMENTI.SM/ADSLARSFSVOFKODSOG TYRKKKKETJAGLIAANUVLJPUVTANIVOGLIAANIVIITOTHERALA II DPROVIENTIKAPAGERTTOPRSSREGTI
6119	1217	462	EKEBENTKOKENNENERGPKOGEKORKOSTLTETFLEPLEK KOKLIVIGIOGAKTSVILISLANDVORSVAPTOCHEVCINTE DSOMEPLETGOSKPPRGYMENYLSN/ADSLARSPSVOFKODSOP ITWKAKKYLHOLIAANPVLPLVVTANKODLBANYHITDIHEALA II DPRVTENTTKAPAÖÖRTTOPRSSEGGTLENTMEYLSALNFSDL LESVSNISSEKGHKWHYNAPDORPFSVCDIKKTIRKOLTAATT
6119	1217	462	EKERKITKOKKINNEKKOPTKOGESKORNOSTJITRTELEPIEK NOCIJALIOLOGAKTSVILISLASHOVOJENAVPOJENOSTJITRTELEPIEK NOCIJALIOLOGAKTSVILISLASHOVOJENAVPOJENAVITE DEQMEPLIKOGSKOPREVENYISKI/ADSLASSFSVOJEKODSOP THYDAKKYLIJOLANNUPLJAVVINODOLIANIVITDIBELA II DERVITRATKAPADERTTOPRSSEGOTIRSTMEYLISALNFEDL LASVSNISSEGORKUVETNAPPOGREPTAVODIKRTIEKGI/TAATE OKMARAHENILIANUVILIVILEBOTAVISSEFOCIJEDOTICIS
6119	1217	462	EKERKITYOKKSINEKKOPYKOGEKORKOSTIJRTPLEPIEK NOCILAVILLOKOKTSVILLISLANDIVOSTVAPOTOT DOQUEZILLOGISKOPROVENILLISLANDIVOSTVAPOTOT INWENAKTILGIJANIVO, PUVYNODOLIANIVI DIEMAL TIWENAKTILGIJANIVO, PUVYNODOLIANIVI DIEMAL NENDAKTILGIJANIVO, PUVYNODOLIANIVI DIEMAL NOPEVYNENTYKAROGERTODRAS SEGUT. RSYNEYLGIJANIVO OKHARAKITILLINOVILTULEBUGTAVESED POLIZBOTCIJA OKHARAKITILLINOVILTULEBUGTAVESED POLIZBOTCIJANIV
6119	1217	462	EKERKITKOKKINNEKKOPTKOGESKORNOSTJITRTELEPIEK NOCIJALIOLOGAKTSVILISLASHOVOJENAVPOJENOSTJITRTELEPIEK NOCIJALIOLOGAKTSVILISLASHOVOJENAVPOJENAVITE DEQMEPLIKOGSKOPREVENYISKI/ADSLASSFSVOJEKODSOP THYDAKKYLIJOLANNUPLJAVVINODOLIANIVITDIBELA II DERVITRATKAPADERTTOPRSSEGOTIRSTMEYLISALNFEDL LASVSNISSEGORKUVETNAPPOGREPTAVODIKRTIEKGI/TAATE OKMARAHENILIANUVILIVILEBOTAVISSEFOCIJEDOTICIS

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRK3FVBAVR
1		1 2/3	VRYVAFRYRTPRAVCLRLWSCRREVINSGRGKQGGKVRAKAKSR
1			SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
1			ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAGG
			G\VLPNIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
		_~~/	RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
1	1	[	KGNGLKAVIPLKPGELLFKSDPLATIVCKGSRGVVCDRCLLGKE
			KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS
1	1		VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
I			QLVMTFQHFMRBEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
1			MQEVGVGLYPSISLINHSCDPNCSIVFNGPHLLLRAVRDIEVGE
			ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
			TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
			PDINIYQLKVLDCAMDACINLGLLEEALFYGTRIMEPYRIFFPG
			SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH
			SLIEDLILLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT LCFVSCVNLSYWKFCSVFV
6122	2	2324	
	-	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG
1			NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL QAAAQSLNVQSKSNBESGDSQQPSQPSQQPSVQAAIPQTQLMLA
			GGQITGLTLTPAQQOLLLQQAQAQAQLLAAAVOOHSASOOHSAA
			GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
			LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN
			LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKR_DTPS
			LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
	i		FSPTTIFRFBALNLSFKNMCKLKPLLEKWLNDAENLSSDSSLSS
1	1		PSALMSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
1			EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
1			VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
i			SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
			AAQLPANASLAANAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
			GALSPALMSNSTLATIQALASGGSLPITSLDATONLVFANAGGA
			PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA
			TSTSAESIQNSLPTVASASGAASTTTTASKAC
6123	3	2944	HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL
	-	27.1	HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
			ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT
( )		ſ	KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
			SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL
			PLCADVVPGPSWEESFWRLTVFFVSLSLLGVTLIAFQQAQYILM
1 1			EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS
1			DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
			HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
J i			SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
1			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
			PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVEHCENLKKVDTK
1 1	1	1	PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
		- 1	QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
		- 1	SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
			KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
		i	VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNFMTGNSLFOY
		- 1	AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
1			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAFP
			EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
1 1	1		QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN
			Z
			•
			450
			100

Deciming   Deciming				
Degithing   Indication   Locati	SEQ	Predicted		Amino acid segment containing signal peptide
Accession of corresponding				(A=Alanine, C=Cvsteine, D=Aspartic Acid W-
Corresponding   Coffree	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first to first residue of semino acid sequence sequence sequence  1573  216  1573  216  1573  216  1573  216  1573  216  1573  216  2174  2175  216  2175  2175  2175  2175  2175  2175  2175  2185  2186  2187				H=Histidine, I=Isoleucine, K=Lysine,
anino acid residue of amino acid sequence sequen				L=Leucine, N=Methionine, N=Asparagine,
residue of maino acid sequence      Mathyptophan, Natyrozine, Xaduknour, *estop     Codon, *possible mucleotide distriction     PITHEND THERMSON WINESPERS WIFFER W				
### and acid sequence   Codon, /-possible nucleotide deletion,    -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEMBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTTA  -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTA   -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTA   -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTA   -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTA   -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTA   -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WILDIWTA   -possible nucleotide insertion   -printheD/THEWBA/WCKEYYEFF WIFFA/WC	1			S=Serine, T=Threonine, V=Valine,
Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6124 1573 236 SEPARATIVES STORY STOR			sequence	Codon, /=possible nucleotide deletion,
6124 1573 216 SEPARLEMENT SERVICES IS SERVIVES FOR PLATITIVE ADALIPERATIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PLATITIVE SERVICES AND ANALYSIS OF PROGRAMMENT OF P	-	sequence		\=possible nucleotide insertion)
6124 1573 236 SIDEALELAGERSMENDENCHTETISTISTERVINYSGEPLATVINVELL GALPPRATURYCIOSGOVERALONDAWYMENG THISSISLADK GALPACHTETISTISTOROGYMENDATAWYMENG THISSISLADK GALPACHTETISTISTISTIANISTISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTISTIANISTIANISTIANISTA TITAINISTIANISTIANISTIANISTIANISTA TITAINISTIANISTA TITAINISTIANISTA TITAINISTIANISTA TITAINISTIANISTA TITAINISTA				
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GSLIAGERS PEOPELLE ATATATE SEGOPESIC THIOWARA HET PER SEMENCIA PULL HIS PLANES IN THE DEGREYA SECTION AND AND AND AND AND AND AND AND AND AN	6124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
SCHMIKESLYPILISPILIANSI (DILEGONYASATEKESYLLINYAS SYVIATSTELIGONYOGAOLAINERSA(MERCA)MEGILIANDIALOGAI  SYVIATSTELIGANYOGAOLAINERSA(MEGILIANDIALOGAI  FOCALITIETYICANIA (PRIVATA) (PRIVATA) (PRIVATALOGAI  FOCALITIETYICANIA (PRIVATA) (PRIVATA) (PRIVATA) (PRIVATALOGAI  FOCALITIETYICANIA (PRIVATA) (PRIVATA) (PRIVATA) (PRIVATALOGAI  FOCALITIETYICANIA (PRIVATA) (PRIVATA) (PRIVATA) (PRIVATALOGAI  FOCALITIETYICANIA (PRIVATA) (PRIVATA) (PRIVATA) (PRIVATA) (PRIVATA)  FOCALITIETYICANIA (PRIVATA)				GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
SVULTASTOLIGOTY/OGAL-GLAND/ENGSKETTSPY/ASLIJOKY SYNAKSHI HOPYTLAYSLAG PERTYTLAYSLAG PE	1			GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF
SYNAMEN HENVETLARVEGGOVIANCESCHEGUTVALPOSAL POCALIHITY/TUTALVALVALESCHEGUTVALVALESCHEGUTVALVALVALESCHEGUTVALVALVALVALUS VIRGERIAN AUGUSTE POCALIHITY/TUTALVALVALVALVALVALVALVALVALVALVALVALVALVA	ł			SKUHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG
POCSELIHIDYLIQUISLA PERTUTLIFY FOR TAY // THOCHES PPA REPARAMONE PTOOR   SERVICE PREAR PRACAGAGINETINE PYLICITES HEROADISCH PTOOR   SERVICE PREAR PRACAGAGINETINE PYLICITES HEROADISCH PTOOR   SERVICE PREAR PRACAGAGINETINE PYLICITES HEROADISCH PTOOR   SERVICE PRODUCT   FOR THE PHONE PHONE PART   FOR THE PHONE PHONE PART   FOR THE PHONE PART   FOR THE PHONE PART   FOR THE PHONE PART   FOR THE PHONE PART   FOR THE PHONE PART   FOR THE PHONE PART   FOR THE				SVVLTASTDLRGYVVGQALQLHADVENQSGKETSPVVASLLQKV
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6128 1 904	1			PGCSEIHIDYYLQVSEKAPEATVTLPVFIGNIAV/NPCPSEPPA
6125 1 904 KICHELTCREFT VER VERBEGGGGGVER 6126 1 904 KICHELTCREFT VER VERBEGGGGGVER 6127 KICHELTCREFT VER VERBEGGGGGVER 6128 KICHELTCREFT VER VERBEGGGGGVER 6128 KICHELTCREFT VER VERBEGGGGTVER VERBEGGGGGVER 6128 THE VERBEGGGGGVER 628 SERVER VERBEGGGGTVER VER VERBEGGGGGVER 628 SERVER VERBEGGGGTVER VER VERBEGGGGGTVER VER VERBEGGGGGTVER VER VERBEGGGGGTVER VER VERBEGGGGGTVER VER VERBEGGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				HEOROPI LAW SOURCE PROPERTY OF THE PROPERTY OF
6128 1 964 KTCPELTCRFTS-VPDSCCEVCRGDGELSBEBSTGD.TRG2ARR EARRISHESHTDPPSSQAGGLS-PFDASSFRGALINGQASGT UND TIMBURGOVCSBECTVESSBEBSTGD.TSG2ARR EARRISHESHTDPPSSQAGGLS-PFDASSFRGALINGQASGT UND TIMBURGOVCSBECTVESSBEBSTGD.TSG2ARR PTOSPAGE SECTION OF THE SE	1	i I		DYPARCECOM TOTAL TO A PROPERTY OF THE PROPERTY
6128 1 994 KICPERITORITYS VPROSCHYCEGOESE PERSISTELT FEDRARS RARSHMEN TOP PROSGONGE PER PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS SPESIMENT PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS SPESIMENT PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS SPESIMENT PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS SPESIMENT PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS SPESIMENT PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS SPESIMENT PAGAS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITYS REGALINGOASOT LYOLYTINICHIRIO VYENNICITY REGALINGOASOT LYOLYTINICHIRIO VYENNIC	1			POT TORCO
RARSYMESTIC PRODUCT FOR THE TOTAL THE CONTROL OF TH	6125	1	904	
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6126 1224 389 RILSBERGPERBERGPERBERGPERBERGERGERGERGERGERGERGERGERGERGERGERGERGE	1			PGOSFDNKGYFCGRETMPVVRSVFMPDGETTPVTALPTPRDDOV
6126  1224  SEPTION OF STREET, CONTROLLING STR				EVHVWTIRKGTLOHFHTEKTSKPMFERT DERVIJEDDETT SOMKT
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COVLEARTY KVSCHRIJGHSCLECKRCPCDMTSKY FRÖSK KOPPCPKCHRTOPETHILISHSTELKREGRIGGEDDAS SYDA YWNILSDKYODTS YHBEEDD YEARDDEES DEGRKDSDTESS DLIFTMILIGRY FASCHAITES	] ]			CPLTDAEC\VECKRGVWDHGGRIFSCSFCHNFLCFDDDFFHORS
KOPPCPKCGHETOETKLISKSTRALKPGROTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEEDEYGAEDDEEEDDEGREDSDTESS DLFTNLNLGRTYASGYAHYEGEN	] ]		1	CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKORKG
YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEQEN			- 1	KQPPCPKCGHETQETKDLSMSTRSLKFGROTGGEFGTGAEGVDA
DLFTNLNLGRTYASGYAHYEEQEN			ŀ	YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
6130 3 577 GRGGTMREYKVVVLGSG\GVGKSALTV\OFVTCTFTEKYDDTTE			_	DLFTNLNLGRTYASGYAHYEEQEN
	6130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE

SEC	Predicted	Predicted end	District Control of the Control of t
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	mo quono o	\=possible nucleotide insertion)
			DFYRKBIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
1 1		l .	ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD
			LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQ
1 1		ì	MNYAAQPDKDDPCCSACNIO
6131	3	1811	SS PREXTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS
	-		PRSLSAMRLLPLAPGRERRGSPRHLPSCSPALLLLVLGGCLGVF
1 1			GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
l i			SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI
1 1			QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
1 1			SYMYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL
1 1			DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN
1 1			KNFNIHGTNKHWLIRQAKTFMTMSSICFLDNAFRKRWQTLLSVD
1 1			DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKRQLY
1			EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
1 1			TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
1 1			PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDQEVFV
1 1			EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT
1 1			PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
1 1			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
i 1			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
			FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRF
			SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
1 1			ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDBLFKLAPEKVNA
i I			VKEAIVNFVMQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
1 1			LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
l i			TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGBMADTDLFMECEEBELBPWQKISDVIEDSVVEDYNSVDKT
1 1	ľ		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
l i			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
1 1			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
i l			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1 !	1	i	TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGOSPGPVVVSNNSSAF\
]			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1 1	1		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
1			/THPSSTPIPALSPPY/TKVPEPNENVGDAVOTKLIMLVUDFVV
1 1	1		GROGGKVAQLINFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1 1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKOLEGLKPGTKVTIRA
			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
1 1	J	I	IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSDCRYST
		1	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1	ļ	1	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1 1		1	NVKNMYPPPSFPTNKAATVKSAGATPAEPERLLTPLAPALPSPA
1 1		1	STATPPPTTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
] ]			
1 1		!	LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPO
			RRIERWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTOREOOLP
			RRIRRWLRRFQASQGENLEGKYLS FEAEEKLAEWVLTOREOOLP
			RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			RRIRRWLRRPQASQGENLBGKYLSFEAEEKLAEWVLTQREQQLP VNEETLPQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
			RRIERMLERPOASQUENDOGKYLSFEAEEKLAEWVLTOREQQLP VMEETLPQKATKIGRSLEGGFKISYEWAVRFWLRHHITPHARRA VAHTLPKOVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLPL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILAGGTVLPTLVFY
			RRIRRWLRRPQASQGENLBGKYLSFEAEEKLAEWVLTQREQQLP VNEETLPQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peotide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
	bequence		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
1			DVC1KR1VKNF EHKKWKEQWKEMADTACDSDVLLQLVLVWLGEV
		i .	LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
		Į.	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
61.34	2		FYGFEEADLDLMEI
6,1,34	2	4256	FVHGSMADTDLFMECEEEBLEPWQKISDVIEDSVVEDYNSVDKT
l l	J.	1	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
1	1		IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASPVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
		1	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
	Į.	l	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIR3MNHMKHHVE
		l	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICHWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
- 1		1	VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYNRHQKR\NVYH\
			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
			IQKRAVRKMSVMGRQTCLECSFEIPDF?NHFPTYVHCSLCRYST
- 1			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
			NVKNMYPPPSFPTNKAATVKSAGATPAEPBELLTPLAPALPSPA
ľ			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
			LASGGGGSGCVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
			RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
	100		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
			ROUGHI INDCHOMIN COMMINING COCCUR DANNING COCCUR
1			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
			FYGFREADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEBEBLEPWOKISDVIEDSVVEDYNSVDKT
			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSOMTPVRPG
1			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPFAVSIASPVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
		ĺ	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAOFRVTEAL
	J		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPMENVGDAVQTKLIMLVDDFYY
	J	ſ	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1 1		4	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
		J	KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1 1		J	CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1 1		ļ	SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLFVFLYPPVQRS
1 1		J	IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	K-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide inscrtion)
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALDSDA
1			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
1			LASGGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1	ĺ		RRIKRWLRRFQASQGENLEGKYLSFEABEXLAEWVLTQREQQLP
1			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENACLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
1	i		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
			RGOMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWOKHTACO
1			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
1	İ		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
i			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
6136	1704		FYGFZEADLDLMEI
9136	1704	539	FGVRMALBGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
1			SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
			DLEEEIHQKQGQKRKNSOPGVKVADRKILDDTEDTVVSQRKKIQ
1			INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
1			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
1			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVBESAIEK
1			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKORKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
			MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
1			YLWOG\LFQLYLDEAGRGHSFSFHGAALTAFKQGQELMAKALES
1			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ
1			LQHAGLRBAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
			LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL
			PFRDQNRKALDGLWNRHHVERVEIINKETVDAEGRTSFYEEYGV
í			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
			QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
			RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
1			QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
			LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
			LASWNFWTPLLESLAHKAPRLYPGGAENGRILDFEFSSGRLFFS
			QQQPRQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
1			ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
l i			AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
			TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV
			AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
	Į.		DAFLG
6138	4587	934	BFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
		J	TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
	1		TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMBPQLAEMIKQ
1 1	1		FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
i l			ELIKELEOSLASWTQNLKELQTMKADL/TRHVL/VEDVMVLKEOIE
	!	l	HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
			ENKVLQTADISIERMIEKLQKDCMEBINLFSENKLQLKQMGDQL
1		1	IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI
	l.		QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD
			LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
		i	LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFBDWLKSAE
			RTAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY
			RRLARBNRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT

SBC	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y-Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\-possible nucleotide insertion)
-			
			NOREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG
			FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEBLHR
			YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
1			DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
1			WDHTGRRGGPSSSH\EECEEAQYY\SALSGKSISDGHSWHVPDS
			PSCPEHHYKOMEGDRNVPPVPPASSTPYKPPYGKLLL?PGTDGG
	ĺ		KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
ł			LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
1			LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
1			LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
1			SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
1 .			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKÇLREQVSQDLM
			ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
			GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLLACLL
6139			PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
0133	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
1			TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
			YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
1			TORFLSQHRCGEPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL
			IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV
			RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
			PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
1			LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA IRGDHAVTSP
6140	694	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAOPLSVTVWAP
1		250	RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
			SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
			FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
			ARRIRRATOVRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
1			ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFRIS
			PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
			KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIRSI
			NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
1 1			AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
1 1			VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
6142	116		DEFVFDVWGVIGDAKRRGL
0112	116	602	EAEGEQVCGAKCCGDAPHVENREBETARIGPGVM8SKEERALNN
1 1			LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
1 1		J	FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
6143	2802	270	REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
0143	2002	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
1			\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
1 1		j	LLLNEWBASKCNIVCTOPRRISAVSLANRVCDBLGCENGPGGRN
1			SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
1			QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
1 1			YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIBGAVLI
1			FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
1 1		J	TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
1			QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
1 1	1	1	YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPOLOVISN
1		I	AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
		- 1	GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
			GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Fhenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	N-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
i	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			LIKLVKAAGFSSSTISTSWEGNRASQTLSFQEIALLKAVLVAGL
1			YDNVGKIIYTKSVDVTBKLACIVETAQGKAQVHPSSVNRDLQTH
			GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
			IQIITELIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
1			VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
			VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
			FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
1			QDYADNIKAQLFETSSKTGQSVDELFÇKVAEDYVSVAAFQVMTE
1			DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
			GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
1	i		DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
1			QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
			\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPOD
			/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
		1	EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTIS
			L
6146	428	781	LKKKGKEKABAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
			R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
6147			BIVTKERHREINKQATRGDCLAFQMRAGLLP
014/	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
			GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
			ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
1			DEMDRIATIONAVITOFSARISATLQDRHERITKLAGVHALLRKL
1 1			QFLFELPSRLTKCVELGAYGQAVRYQGRACAVLQQYQHLPSFRA
1 1			IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
			SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
1 1			ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
1 1			EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
			GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
			CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
1 1			RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
1 1			RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
1 1			VEDTTAIDVQVLPRLAGVALTQAGGTVPSKGAGAAEDHWQSLPG
1 1			GGDMCINASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
1			CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
63.00	5000		CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
1			KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
1 1			SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
1			PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
1			SSTLSEDOMSRLAKLTKAHROGHMVKVDWLDRLTFREIEMINES
1			VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
1 1	1		LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
			LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
}			DLPQGAKQALALIGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
1		ļ	LRQADDEDLLMYLLQLVQALKYENFDDIKKGLEPTKKDSQSSVS ENVSNSGINSABIDSSQIIT/SAPPPSVSSPPP\ASKTKEVPDG
1 1	i		
1			ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
		ļ	KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
1 1	İ		IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD
1			
	ı		QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

SEC	Predicted	Predicted end	7-1
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /-possible nucleotide deletion,
-	sequence		\=possible nucleotide insertion)
1			PVAEVLDTEGSIQNFFRKYAPSENGPNGISAEVNDTYVKSCAGY
		ļ	CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP
		1	MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
f		ſ	SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND
			ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
1			GHRPLLMDSEDEBEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
1			GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ
1	1		POQEKNEKNLPOHRFPAAGLEGEEFDVFTKAPFSKKVNVQECHA
1			VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
			FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
	1		STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
1	1		VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HQGL
1			S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
			LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIETEIDHDVMTEEKLHQINNFWSDSEYR
l	ł		LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
	1		QEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
		5.1.2	TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAFG
			QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
			KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
			DMK/ DOKKDAMA DA DMOCKLA SAKARAMANA DA SAKARAMANA DE SAKAR
1			PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
	l		KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC
			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
6152	1366	648	GKTDSRERKSOGPFCSTPVSTVLLMIHHPGEFNPADVN
	1 200	040	NRTWSTPSTWMGVALPPLCSTGPWPVTRQTTARTTCGAVPAKCP
1 1			PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
			GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
			KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW
1 1			LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
6153	2	3368	NGEPLAAEKEQPGGAHNPFKD
0133	- 4	3368	GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH
1 1			PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1 1			TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
1 1			YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
			AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
			GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
	1		ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
1 1			WLANFTFASGNEGGYPHIETDAQTNEGIVTLIKEVDYEEMKNLD
	[		FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
			SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
	l l		ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
1 1	l		TGTVLINVEDINDNCPTLIKPVQTICHDAEYVNVTAEDLDGHPN
			SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
1 1		J	FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
		J	AAIALMILAFLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
[ [	i	J	WNNECAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS
1 1			SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE
1			TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
	l l	1	ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL
1 1			KFKTLABVCLGQKIDINKRIEQRQKPATETSMNTASHSLCEQTM
			VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK
			VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSOPOSLIV
			TERVYAPASTLVDQPYANESTVVVTERVIQPHGSGSNPLEGTQH

6154 3660 2146 KKRYEMBERJOCHTOKEN STABLIONVORLOLITÖKE  SITNALIKSI RITSILISI JOASESSAROSSORDE ROADMINNIN  SITNALIKSI RITSILISI JOASESSAROSSORDE ROADMINNIN  SESKIHLIMITARIN LITSILISI JOASESSAROSSORDE ROADMINNIN  SESKIHLIMITARIN LITSILISI JOASESSAROSSORDE ROADMINNIN  SESKIHLIMITARIN LITSILISI JOASESSAROSSORDE ROADMINNIN  SESKIHLIMITARIN LITSILISI JOASESSAROSSORDE ROADMINNIN  SESKIHLIMITARIN LITSILISI JOASESSAROSSORDE ROADMINININ  SESKIHLIMITARIN LITSILISI JOASESSAROSSORDE ROADMINININ  SERETLANDYTYKINGLE REKEISTATIVISYON EVANERI KUL  NISOBELONSARODREVIS SESTORDEVIS KULTURIS SESSORDEVIS LITSILISISI JOANESSAROSSORDE ROADMINININ  ROOSSOTVIS BALANGEVERS SESTORDEVIS LITSILISIS LITSILISIS SESSORDEVIS LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LITSILISI LI	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of santon acid residue of santon acid residue of santon acid residue of santon acid sequence control of the santon acid sequence con	NO:			
to first amino acid am				
amino acid residue of amino acid sequence control of the control o				
### ### ### ### ### ### ### ### ### ##				
amino acid sequence  Codom, /=possible nucleotide deleticm, /-possible nucleotide insertion)  LQDVPYMYRERSEFIASSGVQFILMENIA/NGRNYTIENY APASTIGSS(V) PTERMSTRANTYSGAVEVE DETPOLESSIGN SISTITUSE'N VTENTY VON TYS CAPPED PLEFOLESSIGN SISTITUSE'N VTENTY VON TY COMPANY DE TOUR SERVICE SISTEMATION OF THE SERVICE SERVICE SISTEMATION OF THE SERVICE SE				S=Serine, T=Threonine, V=Valine,
Sequence				
LODDYPYWYRERSETARS SSWYPTLIMBYLIVGGROVPY LEVEL POFICES SINSTITUTES TRYVERS TYPE AS SSWYPTLIMBYLIVGGROVPY LEVEL POFICES SINSTITUTES TRYVERS TYPE AS SOME AS SINSTITUTES TRYVERS THE ASSET OF	1		sequence	
ARASTIGSSYOLPTERSKTARNTYSGAGYPGILPTELESS  6154 3660 2146 KKKTHMSTLQKTVNROMPKPSTBUSKLLQWYSKLDLTDKK KKKTHMSTLQKTVNROMPKPSTBUSKLLQWYSKLDLTDKK KKKTHMSTLQKTVNROMPKPSTBUSKLLQWYSKLDLTDKK STTAHLTSHI IST SILNGLQASEADSEGGED EXAQDEMOND BESKLDHLTDRINGLI SKEGKSSSALLEBRYVALDTVI SKYPI  SPERIANDT SILN SEDTYPTELEVINGLYGKENTYKLDVI SKYPI  BESTLANDTYPTKYNKLLBEKSKLLATURYSGY SEVARENT ILL  NINSDELLGASRADKRUWW SIG GGOPHETILKEL FISBOTTEAN SPHIPADEROVAESLATVABESGGS SVELEKPPTVUVDSKY EKKYVEVNDEKARPPSGSUSHSAT I PLPYLLIMATHGELGI "QUSS ROQSSYTVSSPLANDERVSE SIGSTOSTITUVGWAGSLODJOK EKKYVEVNDEKARPPSGSUSHSAT I PLPYLLIMATHGELGI "QUSS ROQSSYTVSSPLANDERVSE SIGSTOSTITUVGWAGSLODJOK EKKYVEVNDEKARPPSGSUSHSAT I PLPYLLIMATHGELGI "QUSS ROQSSYTVSSPLANDERVSE SIGSTOSTITUVGWAGSLODJOK EKKYVEVNDEVNDEVNDEVNE SIGSTOSTITUVGWAGSLODJOK PIKAAKKIP SIGSTOSTITUVGWAGSLODJOK TOOTTIP I QUVE YMW SIBA RODDIML I LAKRAMINDEVOLGA  TOOTTIP I QUVE YMW SIBA RODDIML I LAKRAMINDEVOLGA VEIGHNEGOUG I YTTVYKYW SIBA RODDIML I LAKRAMINDEVOLGA VEIGHNEGOUG I YTTVYKYW SIBA RODDIML I LAKRAMINDEVOLGA VEIGHNEGOUG I YTTVYKYW SIBA RODDIML I LAKRAMINDEVOLGA ALSSSLEDDIL JOKOVOV VOVIJNIMET CIR RAFOKALKS I PLOG SISSENTOLLOG VOVEVNOLIMBET CIR RAFOKALKS I PLOG SISSENTOLLOG VOVEVNOLIMBET CIR RAFOKALKS I PLOG SISSENTOLLOG VOVEVNOLIMBET CIR RAFOKALKS I PLOG SISSENTOLLOG SIGNAMIN SIRA RODTOTI SIG I RESI-AMPITANO ANTAS PROFILE SIGNAMIN		sequence		
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6154 3666 2146 KKKFMMSTLQFTVRNAMPKSTTSDESHLQMVSKIDLEDNES STPAIR ISI I ISI ISI INIQAGSABADSEQUED RAQUEDNOM BESKIDHLTNINNELL I SKEGNESSALLERINVIADLY I SKYVS STPAIR ISI I ISI ISI INIQAGSABADSEQUED RAQUEDNOM BESKIDHLTNINNELL I SKEGNESSALLERINVIADLY I SKYVSI ROKER CHTBECLATUS FORKERLANDES LANDEN SKISSSOS BERNINDER SKERNER SKERNEN SKERNAMEN SKYRSSISSOS BERNINDER SKRIPT SKRIPT SKYRST SKYRST SKYRST SKRIPT SKYRST	1			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
SPEARING ITS LINGLOADSESANDERS GODER RAD ADMINIST BESKIPHINTERNEL I SEED SESS LILBERNY SAULT VI SKY VIS SPEARROI BY U.S. BETTY ELECTRONIC SECTION AND ADMINISTRATION OF SECRETARY SECTION AND SECTION OF SECTION AND ADMINISTRATION OF SECRETARY SECTION OF SECTION AND ADMINISTRATION OF SECRETARY SECTION OF SECTION AND ADMINISTRATION OF SECTION				SNSTITTSSTRVTKHSTVQHSYS
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BEBTIAMYTPTXYMIGLERKKELBATYGTYSGS SKVAKKRILLU NINSDELLINSRADORDWIS SLGGOPHETILISEL PESISOTEAL SPPHPADEBOVAESLOTVABEBSGSSPSVELEKPPPVWYDSKY EKKYVEWYDLARAFORSONENSA I LPLYLLINSRADIGSLOGOLOG BEKYVEWYDLARAFORSONENSA I LPLYLLINSRADIGSLOGOLOG BEKYVEWYDLARAFORSONENSA I LPLYLLINSRADIGSLOGOLOG BERYLSANDY COLERGY SAMATYR SKYLINSRESKESSERS ROGSSYTVSBP LANGEWRST SISTEMSTITUTUSVAGSLOGOLOG BERYLSANDY COLERGY SAMATYR SKYLINSRESKESSERS BEST LASHY COLERGY SAMATYR SKYLINSRESKESSERSHED BEST LASHY COLERGY SAMATYR SKYLINSRADIGSLOGOLOGOLOGOLOGOLOGOLOGOLOGOLOGOLOGOLO				SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPOIK
NISOBELLONSALDERLOWES I COGNIFICATIVE PERSONDERLA SPPHPADERS CAPES CONTROL THE CONTROL SET OF THE CONTROL SE	, ,			RGKRRYCNTBECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
NISOBELLONSALDERLOWES I COGNIFICATIVE PERSONDERLA SPPHPADERS CAPES CONTROL THE CONTROL SET OF THE CONTROL SE				EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL
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				IITGTPILTFVKDPOLEVNFYTGMDEDSDIAFOFRLHFGHPAIM
				NSCVPGIWRYEEKCYYLPFEDGKPFRLCIYVRHKEYKVMVNGOR
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanina, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEAALRGLIGALTSTPYSPTQHLEREQALAXQFAETLH-TLRFD
1			ELKMINPAIQNDFSYYRRILSRMRINNVPAEGENEVNNELANRM
			SLFYABATPMLKTLSDATTKFVSENKNLPIENTIDCLSTMASVC
			RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
		i	TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
			KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRIMIGPRVAVSILCEDGISH*LLEKH*
1			KSHVLEPLSSLALEBQCLALSLDWSTGKTGRAGDQPLKIISSDS
1			TGQLHLLMVNETRPRLQKVASWQAHQFEANIAAFNYWHPEIVYS
		1	GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
1		1	GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
1	I	1	RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
1		1	ARPOSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
		1	LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKOHVRCOKCLEFGHWTYE
			CTGKRKYLHRPSRTABLKKALKEKENRLLLQQSIGETNVERKAK
		1	KKRSKSVTSSSSSSSSSSSSSSSSSSSSESEETSTSSSSEDSDTDESS
1		i	SSSSSSASSTTSSSSSDSDSDSSSSSSKQ*HQHR*QL*R*TTKEE
			EKEI ELLHS YWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTONTGKARIMILLSVSLGRHWAFTYKFFL
1 1			TPVVFVFFFFFFHRKE*VMQKNFMKSREDEWMEKLNNLHVQRAD
			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
			MILKGQIQBAIALINSLHPELLDTNRYLYFHLQQQHLIBLIRQR
i l			ETEAALEFAOTOLAEGGEESRECLTEMERTLALLAFDSPEESPF
			GDLLHTMQRCKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRILCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1 1			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
1 1			LMQTVYSMAPFPPPQLAELREKYTYNITPFPATVKPTSVSGRHS
1 1			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
			PNBEQSLRSNNIAELS PGAINSCRSEYHAAFNSMMMERWTTDIN
			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1 /			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1 1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1 1			RAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1 1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1 1			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
6165	90	405	GGERFG
0762	20	405	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
1			SCISRTAPRILCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
		ſ	VARLSTGIPKEWRRKVWLTLADHYLHSIAIDNDKTMRFTFNERS
			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
1 1	i	1	WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
1			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
1 1			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLOSHR
	1	1	
			LMQTVYSMAPFPFPQLABLREXTYNITFFPATVKPTSVSGRHS KARDSDBENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE

Deginning   Decision   Cocation	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Location   Corresponding   Labettine, Islanden, Islanden, Nasparagine,   Corresponding   Cofirst   Samino acid	ID	beginning	nucleotide	
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\-possible nucleotide insertion)
			ORMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
1	l		FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
			SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
			LTEVGPRFELKLYMIRLGTLEOEATADVEWRWHPYTNTARKRYP
1			LSTE*AAPRPLGOLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
1	1		LOHORIHTGEKPYCSVCGKAFSOSSVLSKHRTIHTGEKPYECN
1	ļ		ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIOHQ
			RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
	1		TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
			HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
1			MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
			MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
			LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
Į			DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEOEREEEO
i			APLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
			GEDDKPLPTSKPRKOYKMAKENRGDDGATERPKKAKEERRMDOM
			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
1			SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
1			DGVLLGPPGKEGLSVKEPOLVWGGDANRPSAFHKGGSRKGIT.YP
1 1			KPKACWVSPMAKVPAESPTLPPTPPSSPGLGSKRSLEEEGAAHS
			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
1 1			PSPMAAGLMHFPPTSFDSALRHRLCPASSAVHAPPVTTYAAPHF
			PHLNTKL
6176	1040	402	PLSALRAMAEVHVIQQIIGASGFSESSLFCKWGIHTGAAWKLLS
			GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
1			SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
6177			RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
61//	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
	1		CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
			PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRP?
6178	1027		VCPI
61.18	1027	254	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
1	1		LHLATPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
1	i		NIFREQVHLIQNALIESRIDCQHRCGIFQYETISCNNCTDSHVA
1 1	1		CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
6179	806		THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
01/9	806	276	RGETREMAGNLLSGAGRRIMDWVPLACRSFSLGVPRLIGIRLTL
1 1	1		PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
			WKGNBLQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHPNRHGK
6300	3.55		FR*KRKLRTSEKAHLSPWRRETVLFFVRKRLCIFSVIKWGFFG:
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECQN*
, 1			SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
1 1	1		SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
-			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalaniae, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\-possible nucleotide insertion)
1		l	GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
1			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
1			VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
			HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
	ĺ		KENFKVHPAHKVAMILDPQQKLRPVFPYQHEEIIGKVCELINEV
			KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
			PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVFAVGARSGCVN MCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRILLSPVLLPGPRWKPWRRRPMGPLALPAWLQFRYRKNAYLFI
1	1	1032	YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
	l		VSLLELLHIYVGIESNHLLPRFLQLTERIIILFVVITSQEEVQE
			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
1	1		IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
			YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
			KDRLWIQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
			VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFO
1	1	ĺ	VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
	ļ		FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
			CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL
	1		KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
l .			YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
1			SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
1			APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
6183	1118	452	STQT
0200		432	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC GSGCGGCGSSCGGCGSGCGGCGSGCGGCSSCCGCCS
			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
			GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
			CQSSCCKPCCCQ8NCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
			VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
			EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
			FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
			ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
			LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
			HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
1 1			QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
]			NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
			PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
1 !			NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
			TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1			DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI
			NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
1			MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
			FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGO
			QLRKNQOLQRFIQWLKEABEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
			IFFILFGTLLYFDSVLLAFGNLFLTGLSLIGLRKTFWFFFOR
			HKLKGTSFLLCGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
			GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
		1	REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
			GCQEARMQTPRRIGWGWYHTLTLYLWEEK
6186	569	238	VYGIDSSNTNTHGABERNRKLKKHWKLCHAQSRLDVNGLALKMA

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C-Cysteine, D-Aspartic Acid, E- Glutamic Acid, F-Phenylalanine, G-Glycine,
2101	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bodannen	\=possible nucleotide insertion)
		<del>                                     </del>	KERKVKNKVKNKADTEEVFNNSPINGEKMPTSAILPDFSGSVIS
			NIRNOMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSOOI
			PNRETSEANKERRKWTSKSSESNIYSPLTSFITADSELHDIIKD
			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
			EFENOHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
			AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
			LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFKMLK
	1		VVLAPCIET_ILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
			VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
			PSGSRVGSRYD
6187	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHNEPKASCPA
020,	1 2703	****	AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
	1		ERAKHPYS PQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
			LLVAPLDANTLGKVASGICENLLTCVMRAWDRSKPLLFCPAMNT
			AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
			GKIGGYPHLLNGGPALS_PRGQACSRLNWTEGPGLSFFQPGEAA
			A
5188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW
			NIGVFICIRCAGIHRNLGVHISRVKSVNLDOWTOBOIOCMOEMG
			NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
	1		INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPCKKEDPOLP
			RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
			PSPSSSGSRKVVGSMPTAGSAGSVPENINLFPEPGSKSRFIGKK
			QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
	1		PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
			AGMNFYGANGMMNYGQSMSGGNEQAANQTLSPOMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL
		J	TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
			RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
	1		VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
			RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
		1	AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR
		l	GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLOLLDIAGNO
		1	LTEIPEGLPESLEYLYLONNKISAVPANAFDSTPNLKGIFLRFN
			KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
	1		ERERDEVEERETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
			GLHCETCKBGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
		1	VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
			CQEMSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
		1	SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
		1	PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
			KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
			TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
			YQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
	]		VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHEGIKPSMH*LFFLMLSFPHLTPQOPKCPS
			MIDWIKKIWYIYTMEYYATIKRNEIMFPAGTWMBMBAIILSKLM
			QDYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYARDSBPRSDGRAGIRAVGSAARE
			KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
- 1	l .		PEADDPKDNTEARKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIOKLYBRKIKEGMDMNYIIORKKBFRNPSIYEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAOKIEMDKLEK

SEQ	Predicted	Predicted end	Design and the second s
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I-Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKO
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGTEAVGSAARE
1	1		KGGLVSDAYGEDDFSRLGGDEDGYBEEEDENSRQSEDDDSETEK
	i		PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI
	Ī		QFCAIDELGTNYPKDMFDPH3WSEDSYYEALAKAQKIEMDKLEK
I			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
i			DON TOUR TOUR OF THE PROPERTY
			DSAIPVTTIAQPTILTTTATLPAVVTVFTSASGSKTTVISAVGT IVKKAKO
6194	3	950	
0234	] *	350	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1			KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
1			PEADDPKDNTRAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
l .			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
}			QFCAIDELGTNYPKEMFDPHGWSEDSYYEALAKAQKIEMDKLEK
1			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1	ì		DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
1			YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
			PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
			PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
6196	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLOEEDSH
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
			HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL
			FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
			MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
	1		NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
1 1			NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPFNTSLFIRNVADATRPEDLRREFGRYG
	i		PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
			RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS
			RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
i 1			SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
			RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
			YRHKNSW
6198	111	1912	
1		2222	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLODSQ
			REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
l i			MACGVEWFSGIGHTWSQNATNEVSSLETEEKQLEPTAWLDSGTW
I	i		GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
			SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP
1			TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
			AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
	1		DIPGLVRKNRYKTILPMPHSRVCLTSPDPDDPLSSYINANYIRG
1 ]	J	J	YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
	1		EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
<b> </b>	1	j	GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII
		ļ	VHCSAGIGRTGCFIATSICCOOLROEGVVDILKTTCOLRODRGG
			MIQHCEQYQFVHHVMSLY3KQLSHQSPE
6199	144	1211	MARENGESSSWKKQARDIKKIFEFKETLGTGAFSEVVLAEEKA
		J	TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
			ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
			YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKSD
	l		VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, N=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
			FYDENDSKLFEGILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
f			NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
J		J.	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
			HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
1			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
1			QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIONGMNLOTLS
			QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
1			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
	I		RKRILGSASPEEEQEKPILDRPTRISQPEDSROPMVIROPLGP
			DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKKAPOKDRKPKRSTWRFNLDLTHPVE
1			DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
			KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISO
			DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAAPASOHPA
			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA
1			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
1			PILSHELSLLDBFYKLVDPERDMSLRLNEQYEHASIHLWDLLE
			GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
1			SAPAVEDQVPEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFTS
1			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
1 1	ĺ		PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM
1			NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
	ļ		EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNNNAPVP
1 1			PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
1			TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
1 1			RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
			RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
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	į į		PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
	J		RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP CDCQTWKNWLQKITEMKPBELVGVSEAYEDAANCLWLLTNSKPC
1 1		1	ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
		ļ	YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
1 1			NHEHSYQLECRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
1 1		j	HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
1 1			AQKVNRPYLRTPRHKI IKAACLVQQKRQEFLASVARGVAPADSP
1 1			EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRREHQRRRGDVHS
1			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
1 1			SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
		1	LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
1			LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
1 1	1		AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
1 1			CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
			PGGGKOHPOAW
6205	1	1200	RAHRGKMALEVGDMEDGOLSDSDSDMTVAPSORPLOLPKVLGGD
1 1	1		SAMRAFONTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
1 1	1	1	KRQKCFNPPPKPEPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
		i	QDAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESOBHTKD
		1	LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN
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Deginning No: Not location corresponding to cation corresponding to first amino acid acid acid acid acid acid acid acid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note	ID			(A=Alanine, C=Cvsteine, D=Aspartic Acid R-
Context of Corresponding   Coling Contemponding   Coling Contemponding   Coling Contemponding   Coling Co	NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine
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amino acid residue of amino acid		to first	amino acid	P=Proline, O=Glutamine, R=Arginine.
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to Eirst	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ì	(=possible nucleotide insertion)
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKTTCSAHREPRLV
			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRET.QCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
	*		SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEO
			HMCDCDURAL CASI CDCDOUDGUTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
			RPTIPBESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEKKCN
			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAOV
			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
			ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
1			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
- 1			EMNSCLNADDLDLMNSSGGHSEPH
5211	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
			SVICNOLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
- 1			CYUDGWGKUGNGTHOO DE GURGGDGGON FURN THE GREATHD
			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFSEG
			SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
- 1			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
			LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
			GGDIFCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
- [			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
- 1			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGANGSLCNSHWD
- 1			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEO
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
			RPTIPEESAVACIESGOLRLVNGGGRCAGRVEIYHEGSWGTICD
			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSDASRE
			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
.1			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
1			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
- 1			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
- 1			
- 1	J		ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
6212			EMNSCLNADDLDLMNSSGGHSEPH
0212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
			RELPFPACHEIGLGARAGSGPPPAPAARESRSRAMEEEASSPGL
	1		GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
	1	1	OKNNCVMPEDVKNFYLMINGFHMIWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
		j	DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
- 1		J	NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
- 1			GPSGPSGPSTSSTSKSSSGSGNPTRK
6213	1	1134	
	-	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
- 1		1	RELPFPACHEIGLGARAGSGPPPAPAARESRSRAMEERASSPGL
			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
			GCSKPHLEKLITGITRILESSPGVTEVTIIEKPPARRHMISSWE QKNNCVMPEDVKNFYLMTNOFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQEEKPHFDSRS

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	N. Deroke-ber V. Deroke, V. Televice
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
			GPSGPSGPSTSSTSKSSSGSGNPTRK
5214	2	460	HBLAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
	1		VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN
			YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVH
	1		IGQLYSTDKLIIENRDMPRT
6215	2	1849	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV
			MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISHFHLDF
1			CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE
1			ANFFTSQMIKDCMKKVVAVHLHCTVQVDDELEIKAYYAGHVLGA
			AMFQIKVGSBSVVYTGDYNMTPERHLGAAWIDKCRPNLLITEST
			YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAGELC
1	1		ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNOKIRKT
J	1		FVQRMMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF
			RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK
1			MQVEYMSFSAHADAKGINQLVGQAEPESVLLVHGEAKKMEF_KQ
1			KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL
1	1		LPEAKKPRLLHGTLIMKDSNFRLVSSEOALKELGLAEHOLRFTC
			RVHLHDTRKEQETALRVYSH_KSVLKDHCVOHLPDGSVTVESVL
1			LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLPQAPS
6216	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPOLGRPMSS
			GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHER PE
i			FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGRSGLKMEVKPPPGRPQPDSGRRRRRRGEEGHDPKEPEQ
			LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPOTKRSRG
	l I		FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
			HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDROSGK
1			KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKOEMOS
	ŀ		AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGG
			GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG
			NQGGGYGGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSGQQOS
I			NYGPMKGGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF
6218	1305	906	SCERRGFINADDLKRFLYKKLPSVEGLHAIVVEDRDGVPVIKVA
		236	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYOV
			VQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPRADRPHORPFL
0213		090	IGVSGGTASGKSTVCEKIMELLGONEVEQRORKVVILSODRFYK
1			
1			VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
			TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF
			VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP
			TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
6220	227	764	RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
0220	221	/64	EQNISLEMSCTIEKALADAKALVERLR DHDDAAESL EQTTALN
			KRVEAMKQYQEBIQELNEVARHRPRSTLVMGIQQENRQIRELQQ
			ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK
			LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ
6221	98		NVH
0221	98	916	RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP
			NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
			AMTLCTTNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK
			YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE
			AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
[			DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL
L			LDLREKRK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine.
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
			PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
1	ł		EFQAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
			SDGQALPEMETHLQTNAEKGTITIQDTGIGHTQEELVSNLGTIA
			RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
1			SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCKEF
i			SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
			WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
1	Į.		PLNLSRELLQESALTRKLRDVLQQRLTKFFIDQSKKDABKYAKF
1			FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
			EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
			EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
1			CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPANVTVLEMG
			AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNOLRAS
			EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
6223	3	715	DAWARTMAGNVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY
			RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
			GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED
			GQPDLGKARDYYTRACDGGYTSSCFNLSANFLQGAPGFPKDMDL
			ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
6224	1	133	QQVHKBQQKGVQPLTFG
6225	3259	938	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
0223	3239	938	LLSCHRLAICKLPFSVESRKTVNGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAGRALYREVTLENYSHLVSLGTLHSKPELIRRLEO
1 1			GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
			QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
1			SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH
1			KKAHSRQKLFTCRECHQGFRDESAL-LHQNTHTGEKSYVCSVCG
1			RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
			TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
1 1			NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK
			NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC
			MKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERFSFQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFFEDKSSYMKH
			NKSTYVHKE. HAGEKPYRCJECARGFSNKSHLITHORTHSJEK PFACROCKOSFSVWGSLLBURTHSGEKPYCKDCERS PSGKST LVYHQRTHSGEKPFVCRECGOGPIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFFDKSSYNKH LRAHLDEKRFPCRDCARGFTLKFNTLITHGPTHSGEEKPFNCKOCE
	·		NKSYFVUKKRIHSGEKPYRCQEGGRIFSNKSHLITHQRTHSGEK PFACQGCGPSYKOSILDMGTHISGEKPPYCKCGCERSFSGKST LVYHQRTHSGEKPFVCHECGQGFTQKSTLVKHQTTHSBEKPPVC KOCGRGFTQKSFFTLHQRTHSBEKPYGCRCGRRFREDKSSYNKH LRAHLGEKRFPCROCGRGFTLKFNLTTHQRTHSGEKPFHCKQCE KSFSLKANLHRQMTHSGSFPKCKQCGRFTLKSTLTHQKTH
			NKSYTVUHRETHSGEKPYRCOECGGFFRKSHLLTHORTHSGEK PPACRCYCKSPSYUGSLLEHRETHGSEKPYCKDERSFRGKST LVYHOPTHSGEKPFVCRECGCGFTCXSTLVHKOTTHSEKPFVC KDCGRGPJGKSTFTLHQRTHSEKFPYCREGGRFFZKRSSYKKI LGRAHLGERFFCKDCGGRFFILKENLTHGRTHSGEKPFMCKCC KSFELKANLLEHQWTHSGERPFKCKDCGRGFILKSTLFHQRTH SGEKPFTCSGCGGFTEKSNLYKENLTHGRTHSGEKPFMCKCCGGRF
			NSSTYVHERIEGOERPYRCOECORGISSMISHILTHQOTHISGES PPRORCOCOGSSESVESSLEHLERTHGOERSPYRCOECORGISSMISHILTHQOTHISGES LVHYGOTHIGGESEPPUCREGOGOPTOXSTT.VHYG.THISGESEPPUC LVHYGOTHIGGESEPPUCREGOGOPTOXSTOTHGOTHISGESEPPUC LABAILDEREPFCEDCORGPTLYFOLTTHQOTHISGESISSYMISH LABAILDEREPFCEDCORGPTLYFOLTTHQOTHISGESISSYMISH LABAILDEREPFCEDCORGPTLYFOLTTHQOTHISGESISSYMISH KASPELAVABLUEGOTHISGESEPPUCACOGOSSETULSET.THJFOCTHISGES MORGHISTOTHOMATICAL MOR
			NISTYVHIKLIHGOERPYRCORCORGISSIKKHILTHQOTHISGIK PAPACRCKONGSISVENSISLHIHGITHGOERPFYCKERGESFFYKST LVYHQITHGOERPFYCKERGOGIFTCNSTI.VKHICTHGESERPFYC NICHRAPLUSTFHARCHESERVITCHCORGERPISCHSSTYNKHI NICHRAPLUSTFHARCHESERVITCHCORGERPTICATURG KEPSILONILLHUGHTHGOERPPICCHCORGERTILSTILTHQOTH KEPSILONILLHUGHTHGOERPPICCHCORGERTILSTILTHQOTH NIKHLITHGOETHSOERPPICCHCORGERTILSTILTHGOETH NIKHLITHGOETHSOERPPICCHCORGERTISCHTHORTHSKE KEPFUCKERGERTISKOLTUPERICCEPPECCORGERTISCHTSKE
6226	. 29	266	NASTYVHKELHGOERPYRCOBCOMGYSWISHLITHQUTHSGEK PPRACRCOCGSPSVRSSLHLIPHQUTSGEKFFCCECE LVTHQWTHSGEKPFVCREGOGOPTOXSTLVKHQTTHSGEKPFVC LVTHQWTHSGEKPFVCREGOGOPTOXSTLVKHQTTHSGEKPFVC LKGHLIGHGEKFFFCEDCGRAFTLKPHLTTHGWTHSGEKPFVC LKGHLIGHGEKFFFCEDCGRAFTLKFHLTTHGWTHSGEKPFVCKCGG RFFSLKGALLHGWTHSGERPFVCNCOGOSSFILKSTLTHFHGTKF SGEKPFTCSGCGGFTWKSNLVKHGLAHSGKQFFVCKCGGGFT KKGALLTHGWTHSGEKFPVCNCOGOSSFIRKSTLTHFMTHSEK KKPFVCQCKCKGGYTKSKGLTVHEKHTCSEPFYECQEGGRKFSNKS YYSHLKKHLHGKERPVCTGVGGGG
6326	29	266	NISTYVHIKLIHGOERPYRCORCORGISSIKKHILTHQOTHISGIK PPACRECKOGSPENSSLEHIRIPTISSERSPYCKEESESFOCKSTE LVYHORTHGOERPPYCHEGOGGIPTICNSTLVKHIGTTHISSERSPYCK KOCKRIPTIGANTHORINGTHICKORGARPHYCHAGESTAWN LGARLIGHERPYCHICGGGIPTICNSTLVKHIGTHISSERSPYCK LGARLIGHERPYCHICGGGIPTIKSPUTTI.THQPHISGISTPHICK; LGARLIGHERPYCHICGGGIPTIKSPUTTI.THQPHISGISTPHICK; SERIPPYCHICKORGOPTHIKSPUTTICHGRIPTICHTHAGEN KKIMILTHQPHISGIKKPYCHVCQUSSWERSELTHHIRI.THKE KEVILGKHIRIPTIKSPUTTICHGUTTICHTHAGENPYCHOGGGIPTISSERVY YYSHLKARHILEKRPUTGUSVERSS
6226	29	266 890	NASTYVHIKE HIGOERPYRCOBCORGISHNIKHLI THOOTHSGEK PPRACRCOCGSSEVROSLICHIERTHIGSEKPYCCECEGESFOCKST LVHYGOTHIGGEKPFVCERGOOGPTOXSTI.VKHIQTHISSEKPFVC LVHYGOTHIGGEKPFVCERGOOGPTOXSTI.VKHIQTHISSEKPFVC LKGRIGFOLGSFTLIGHTIGTHISGEKPFVCCEGGGERPHISGESTYNKL LKGHLIGGEKFFCENGCGRAFTLICHTLTHOOTHISGEKPFVCKCCG KFFSLICHALLEGGFTUKSNILVKHIQLAHSGKQFFVCKXCGGGFT KKSHLITAGENFVCHICOGGSFEKTI.KTHIRTHISGEKFPVCKCGGGFT KKSHLITAGENFVCHICOGGSFEKTI.KTHIRTHISE KFPLOGCKKGGYTISKSDLTYHERIHTCGEPFYECOGGGEKFSKKS TRYSELLGASGERFTSKNILTHISGERFYCHTOGGGGTKFSKKS TRYSELLGASGERFTSKNILTHISGERFYCHTOGGGGTKFSKKS TRYSELLGASGERFTSKNILTHISGERFYCHTOGGGGTKFSKKS TRYSELLGASGERFTSKNILTHISGERFYCHTOGGGGGTKFSKKS
		_	NISTYVHIKLIHGOERPYRCORCORGISSINKHILTHOCHTISGER PPRACRECKOSSPENSSLEHIRITHOSERSPYCKETESSERSP
		_	NISTYVHIELIEGOERYRCOBCORGISSIKEHLITHOCHTISGER PARCACCOGGSVEWSSLEHLENTIGEREFFYCCHEGOERFFYCKEEGGEFFYCKEEGFFYCKEEGGEFFYCKEEGGFFYCKEEGFFFYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTYCKEEGGFFTTYCKEEGGFFTTYCKEEGGFFTTYCKEEGGFFTTYCKEEGGFFTTYCKEEGGFFTTTYCKEEGGFFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
		_	NISTYVHIKLIHGOEKPYRCORCOMGYSMIKHLITHQCTHISGEK PPROCRCOCGSPEWSSLEHIRITHGESEKPYCCECEGSFGWSTLYKHGITHGESEKPYCCECEGSFGWSTLYKHGITHGESEKPYCCECGGRFGWSTLYKHGITHGESEKPYCCECGGRFGWSTLYKHGITHGESEKPYCCECGGRFGWSTLYKHGITHGESEKPYCCEGGRFGWSTLYKHGITHGESEKPYCCEGGRFGWSTLYKHGITHGESEKPYCCEGGRFGWSTLYKHGITHGESEKPYCCEGGRFGWSTLYKHGITHGESEKPYCCEGGRFGWSTLYGWSTLYGWSTLYKHGITHGESEKPCLTGWSTLYGWST
		_	NISTYVHIRLIEGORPYRCOBCORGISSIKKHLITHOCHTISGER PPROCECCIOS PSYRKSILLEHIERTHOGERPYRCOBCORGISFRYCHTISTER LVTHIGHTHSGERPPYCHECGOGPTCYSTILVKHCITHESERPPYC LVTHIGHTHSGERPPYCHECGOGPTCYSTILVKHCITHESERPPYC LVTHIGHTHSGERPPYCHOCGOGPTCHSTILVKHCITHESERPPYC KSPELANGLEHIGHTHSGERPPYCHOCGOGPTLISTTLIFHICHTH KSPELANGLEHICHTHSGERPPYCHOCGOGPTHASTLIFHIGHTHSER KSPELANGLEHICHTHSGERPPYCHOCGOGPTHASTLIFHIGHTHSER KSPELANGLEHICHTHSGERPYCHOCGOGPTHASTLIFHIGHTHSER KSPELANGLEHICHTHSGERPYCHOCGOGPTHASTLIFHIGHTHSER KSPELANGLEHICHTHSGERPYCHOCGOGPTHASTLIFHIGHTHSER KSPELANGLEHICHTHSGERPYCHOCGOGPTHSSILTHHSER KSPELANGLEHICHTHSERPYCHOCGOGPTHSSILTHHSER KSPELANGLEHICHTHSERPYCHOCGOGPTHSSILTHHSER KSPELANGLEHICHTHSERPYCHOCGOGPTHSSILTHHSER KSPELANGLEHICHTHSERPYCHOCGOGPTHSSILTHHSER KSPELANGLEHICHTHSER KSP
		_	NISTYVHIKLIHGOERPYRCORCORGISHMIKHLITHOCHTISGER PPRORCOCOGSPROWSLIHLIHGUSERPFYCCERCESFSGESFTOKET LVYHORTHGOERPPUCREGOGOPTOKSTLVKHIGITHSSEKPPVC LVYHORTHGOERPPUCREGOGOPTOKSTLVKHIGITHSSEKPPVC LAGHLUSKERPFCHOCHROPTLKOPHLITHOCHTISGERPPVC LAGHLUSKERPFCHOCHROPTLKOPHLITHOCHTISGERPPVCKCOG ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGOSTHISGERPVCKCOG ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGOSTHISGERPVCKCOG ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGOSTHISGERPVCKCOG ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGOSTHISGERPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHIGHTOCHTISGERPVCHOCHGORGPVCHOCHGORGPVCHOCHGO ROPTOKSTLVHICHTOCHTISGERPVCHOCHGORGPVCHOC
		_	NISTYVHERIHGOERPYRCORCORGISHMIKHLITHQOTHISHER PPRACROCOGSPEWSSLEHIRITHGOERSPYRCORCORGISHMIKHLITHQOTHISHER LVYHQOTHISGERPPVCREGOQUPTQXSTLVKHQITHSBERPPVCL LVYHQOTHISGERPPVCREGOQUPTQXSTLVKHQITHSBERPPVC LAGHLUGKERPFCREGORROPTLKOPHLITHQOTHISGERPPVCREGORROPTHAGOPHLITHQOTHISGERPPVCREGORROPTHAGOPHLITHQOTHISGERPPVCREGORROPTHAGOPHLITHQOTHISGERPVCREGORROPTHAGOPHLITHQOTHISGERPVCREGORROPTHAGORPPUCREGORROPTHAGORICATION CONTROLLING CONTR
		_	NISTYVHIKLIHGOERPYRCORCORGISSIKKHILTHOCHTISGISK PARCRECOGGSPRISSIKHILTHOCHTISGISK PARCRECOGGSPRISSIKHILTHOCHTISGISK POKUSTIVAKIOTHIS TIRAKIOTHISGISK POKUSTIVAKIOTHIS TIRAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS TIRAKIOTHIS POKUSTIVAKIOTHIS POKUST
		_	NISTYVHIELIEGOERYRCOBCORGISSIKEHLITTIQCTHISGER PARCACCOGGSPEWSSLLEHLETTIGGERFYCCECCEGERFGERFYCCECCEGERFGERFYCCECCEGERFGERFYCCECCEGERFGERFYCCECCEGERFGERFYCCECCEGERFGERFYCCECCEGERFTLWSTLWSGITTIESEERFYCCECCEGERFTLWSTLWSGITTISSEERFYCCECCEGERFTLWSTLWSGITTISSEERFYCCECCEGERFTLWSTLWSGITTISSEERFYCCECCEGERFTLWSTLWSGITTISSEERFYCCECCEGERFYCCECCEGERFTLWSTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFYCCECCEGERFTLWSGITTISSEERFTLWSGITTIS
		_	NISTYVHIKLIHGOERPYKCORCORGISSIKKHILTHOCHTISGER PPORCECKOGS PSYKKSLIHLINGTHISGERPYKCECKORGISPER PGENT LVYKORTHISGERPYKCERGOGIPTCANTILVKHICTHISGERPPYKCE LVYKORTHISGERPYKCERGOGIPTCANTILVKHICTHISGERPPYKCA LGARLIGERRYCHACOGIPTLANTILTHOCHTISGERPPKCACCA LGARLIGERRYCHACOGIPTLANTILTHOCHTISGERPHCACCA KOCKRICHTUNG LOOGOOPTURENLYKOPTCORGORGIPTCANTIL KOCKRICHTUNG LOOGOOPTURENLYKOPTCORGORGIPTCANTIL KOKRICHTUNG LOOGOOPTURENLYKOPTCORGORGIPTCHICTHON KOKRICHTUNGTYSSIKOPTCONTOCOTY KOKRICHTUNGTYSSIKOPTCORGORGIPTCORGORGIPTSIKOPTCORGORTINGTURG KOKRICHTUNGTYSSIKOPTCORGORGIPTSIKOPTCORGORTINGTURG KOKRICHTUNGTYSSIKOPTCORGORGIPTSIKOPTCORGORTINGTURG LINBAGGIGLAVSTOLSHILLIPKING PTEAGRAFTSIGOTOMPTLTIC LOOGOOFTINGTURG LOOGOOPTCORGORTINGTURG ANGARISTANDOSTURGSTOLSHILLIPKINGTURGUNGTURGUNGTURG ANGARISTANDOSTURGSTOLSHILLIPKINGTURGUNGTURGUNGTURG ANGARISTANDOSTURGSTOLSHILLIPKINGTURGUNGTURGUNGTURG ANGARISTANDOSTURGSTOLSHILLIPKINGTURGUNG
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6228	47	1978	GRRCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLRRL
			CLGCGADIWAYILQHVHSQRTVKKIRGNLLWYGHODSPOVRRKL
i			ELBAAVTRIRAEIQELDQSLELMERDTEAQDTAMEOAROHTODT
			ORRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
			DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
			SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
			EABIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
]		İ	RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
1			ILGLERCCLWTELKALHDQSQELQDAAGHEQLLLRELQAKQQRI
1			LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
1			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1			RODLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQEKO
			QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
			ELCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIFFLTIGRRLTGRMAAVDDLQFEEFG
			NAATSLTANPDATTVNIEDPGETPKHOPGSPRGSGREEDDELLG
			NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
			LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
1	Į.		HLGEKTYHYVPEFRKVSIAATIIYAYANLVPLALWGFLMWRNSK
			VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
i :			ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
			AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
			NDEELNQLLKGVTIASGGVLFRIHPELLAKKRGTKGKSETILSP
1			PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
			SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
			TTARIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
			SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL
			KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEC
1			LGVTALSTLYGGMLLSSMFLPPLLIERLGCKCTIILSMCGYVAF
1 1			SVGNPFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK
1 1			ACKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL
1 1			PEEQLT3CGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
6232	3679	1476	AVLMIAAFLQPIRDVQRESE
0232	3075	14/6	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQOLMLSAALRTLKHVL
1 1			YYSROCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
			KKMGIKTVAIHSDVDASSVHVKMADBAVCVGPAPTSKSYLNMDA
			IMRAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
			IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
1 1	i i	,	PVMIKASAGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
1			APSIFLDARTRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
ĺ			INGWAVECRVYAEDPYKSFGLPSIGRLSOYOEPLHLPGVRVDSG
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1 1	1		THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK
	1		NQLLAIASSLEVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
1 1	1	1	DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
1	0	1	TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMONS
1 - 1		i	MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
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LVMLNNLVKAFTEANTGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK				
DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK				
		i i		LVMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS
LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI	1			DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK

SEQ	Fredicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=PhenyLalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Tsoleucine, K=Lvsine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN
			IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS
	i e		KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL
	į		RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAOLGKARLHLKL
			LDYLNHOWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
- 1			YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
			FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
			MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
			KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
			ILLRLDNELGGIIABVNLAEHSTVITFLDYHDGAATFLLINHTK
			NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCRKS
1			HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK
[			VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
			VVWETKPKKKARWKPMSVKHTEKLEREFKEYTESSPSEDKVIQL
			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
	i		SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTR
			AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
1		Į.	IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLLKSIGATLTD
			VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
			GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
			LKALVGGAVGGLAGAASKITGANAKGVAANTMDEDYQQKRREAM
	į.		NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGGAAG
			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
			PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
			DDDDDDDDBSDLNH
6239	2108	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA
	1		THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL
			SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
			FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
			WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG
1			ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
			WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI
1	1		GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPOTDVLLHI
			DVAAAOTGVSR FLOVNSAWRYDKREDVOPGTGMLAYTHILMEAA
1	1		PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
	ļ		ERLPRPS
6240	2202	1176	HERGDSLKEPTS IAESSRHPS YRSEPSLEPES FRS PTFGKSFHF
1			DPLSSGSRSSSLKSAGGTGFELGOLOSIRSEGTTSTSYKSLANO
1			TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
1			AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLOEREKL
1			LROSPPLPGREEEPGLGDSGIOSTPGSGHAPRTSSSSDDSKRSP
1			LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
1			SOKAOPGVSETEEVALOPLLTPKDEVOLKTTYSKSNGOPKSLGS
1			ASPGPGOPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT
			RVERLTFHLLEFPEGKGVAVKERIIPYLLRLROIKDETLOAAVR
1 1			BILALIGYVDPVKGRGIRILSIDGGGTRGVVALOTLRKLVELTO
			KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
			FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
			TCPKVAAVSTIVMRGITPKAFVFRNYGHFPGINSHYLGGCOYKM
1			WQAIRASSAAPGYFAEYALGNDLHODGGLLLNNPSALAMHECKC
			LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD
			TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE
			GLKYIERNBQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP

Seg				
No.   location   loc	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Cofirst   amino acid   tesidue of imaino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   companies   Code,   Code				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid acid acid acid acid acid acid acid	NO:			
to first amino acid am	1			H=Histidine, I=Isoleucine, K-Lysine,
amino acid residue of amino acid amino acid sequence solvente, T-THINCONIN, Y-TYCENIE, X-SURMOND, *-SCOP COdon, /-possible nuclectid election.  **ATTYPEDPOIN, Y-TYCENIE, X-SURMOND, *-SCOP COdon, /-possible nuclectide deletion.  **PSESS	1			L=Leucine, M=Methionine, N=Asparagine,
### ### ### ### ### ### ### ### ### ##	1			P=Proline, Q=Glutamine, R=Arginine,
anino acid sequence  Codon, /-possible nucleotide deletion,	1			
Sequence   Apossible nucleotide insertion	1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
FPSKL  OFFICAMENTS-GRAVICTAREFFOR LAWPEPARAPREAVENCE SSED IOMPSTLIGHBRUITGSLOVTILPPEPARAPREAVENCE SSED IOMPSTLIGHBRUITGSLOVTILPPEPARAPREAVENCE OFFICAMENT AND ADMINISTRATION CONTROL OF STATE OF THE STA	1		sequence	Codon, /=possible nucleotide deletion,
S242   198		sequence		
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SOPVVELVAKVLGACKLLIJELDCCCKTFILITVKHIGLGFFII LALVAWGLVSRIWVLYKOVLKRILLYFPLPGLLOEVARIOPM YPKDFTFSDITTEFIGOPYPEAFRKKMPIAPJAKGIIKKLLKKLF				
Lillvmvglvsrliwvlykgvlkrlillyeplfglloevariopmp yfkdftfpsditeflgopypbafkkkmpiapaakginkllnklf				
YFKDFTFPSDITEFLGQPYPBAFKKMP1APAAKG1NKLLNKLF	j	1		
	1 1			
LINEQSPRASEBTLLGISKKAKQMKINVQNNVDLGQPVKNKRVF	]			
				LINEQSPRASETTLEGISKKAKQMKINVQNNVDLGQPVKNKRVF

SEC	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			KEBSSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAOAI
			FLGNKLLKSNRLKHLEAGGTSLPKKLECIKTSICNHLLRGSGIK
			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
1			HENLEGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	S6	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVCNPGAALDLCI
J	l		AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
	1		ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
1			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
			LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP
1			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
1			LINEQSPRASEETLIGISKKAKQMKINVQNNVDLGQPVKNKRVF
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
	i		FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
1			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
i			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIOTKEKMI
			HENLEGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKQLETVLDD
1			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
1			REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
i			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
			SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
1			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
6251	62		VBGDHQ
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
			PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
			KLCLNIRLAVKEGGPNPBHNSNLANILEVCRSKHMPKSTIETAL
			KMEKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
		İ	NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
1			AEDVKETEDERERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
6252	27	1897	EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYNEE
		2007	
			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKPCRIDKSR
1			KLPHSKAKTRSRLEVABAEEEETSIKAARSELLLAEEPGFLEGE
1			DGEDTAKICQADIVEAVDIASAAKHFDINLRQFGPYRINYSRTG
1			RHLAFGGRRGHVAALDWYTKKLMCEINVMEAVRDIRFLHSEALL
			AVAQNRWLHIYDNQGIBLHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
1			KIFDLRGTYOPLSTRTLPHGAGHLAFSORGLLVAGMGDVVNIWA
			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
1			SMLVPGAGEPNFDGLESNPYRSRKORGEWEVKALLEKVPAELIC
	f	J	LDPRALAEVDVISLEQGKKEQIBRLGYDPQAKAPFQPKPKQKGR
			SSTASLVKRKKKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDREVR
6253	27	1897	ERFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
1 1	1		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
1			KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWYTKKLMCEINVMEAVRDIRFLHSEALL

1D beginning nucleotide (A-Alanine, C-Cyst	t containing signal peptide teine, D=Aspartic Acid, E= Phenylalanine, G=Glycine,
NO: nucleotide location Glutamic Acid, F=I location corresponding H=Histidine, I=Isc	teine, D=Aspartic Acid, E= Phenylalanine, G=Glycine,
location corresponding H=Histidine, I=Iso	Phenylalanine, G=Glycine,
Corresponding   to first   L=Leucine. M=Methi	oreucine, Kebysine,
	ionine, N=Asparagine,
	amine, R=Arginine,
	nine, V=Valine,
	yrosine, X=Unknown, *=Stop
	nucleotide deletion,
AVAQARWEHT TORQUEE	LHCIRRCDRVTRLEFLPFHFLLATASE
TGFLI YLDVS VGK I VAAL	LNARAGRLDVMSQNPYNAVIHLGHSNG
VIDDI DOUVON CERMIN	CHRGGVRAVAVDSTGTYMATSGLDHQL PHGAGHLAFSQRGLLVAGMGDVVNIWA
	RLSGPVHGLOFCFFEDVLGVGHTGGIT
	NPYRSRKQRCEWEVKALLEKVPAELIC
I DDBALAPUDUTON POOR	KKEQIERLGYDPQAKAPFQPKPKQKGR
COTACLUADADACA	HRDKVRQSLQQQHHKEAKAKPTGARPS
ALDREVR	RDVAKOPPONENHEZNEKA LANGES
	CFALRLRAPGSGRPALAFGAAAFAGL
	LLKEYRICMPLTVDEYKIGQLYMISKH
SHEOGRAGIANIONER	PFEDPHHGNGQFTEKRVYLNSKLPSWA
RAVOVEVENTUVALANTA	PPEDFINGNGGFTERRVILNSKLPSWA PPYTITEYTCSFLPKFSIHIETKYEDN
KGGNDALAUMENANDADA	EVCFIDIACDEIPERYYKESEDPKHFK
SEKTORGOT. DUGWDDGUO	QPIMCSYKLVTVKFEVWGLQTRVEQFV
HKYVRDTLLIGHROAFAN	VDEWYDMTMDDVREYEKNMHEQTNIK
VCNOHSSPVDDIESHAOT	
	/ASQKALSVESKAVIKOOLESVSNGWT
	KELYQSLLTQVASKHFYFWLNSLKEFS
HAEOCLTGLOEENYSSAL	SCIAESLKFYHKGIASLTAASTPLNP
LSFOCEFVKLRIDLIOAF	SQLICTCNSLKTSPPPAIATTIAMTL
GNDLQRCGRISNOMKOSM	SEFRSLASRYGDLYQASFDADSATLR
NVELQOOSCLLISHAIEA	ALILDPESASFÇEYGSTGTAHADSEYE
RRMMSVYNHVLEEVESLN	GKYTPVSYMHTACLCNAIIALLKVPL
SFQRYFFQKLQSTSIKLA	LSPS PRNPAEPIAVONNOOLALKVEG
VVQHGSKPGLFRKIQSVC	CLNVSSTLQSKSGQDYKIPIDNMTNEM
EQRVEPHNDYFSTQFLLN	FAILGTHNITVESSVKDANGIVWKTG
PRTTIFVKSLEDPYSOOI	RLQQQQAQQPLQQQQQRNAYTRF
6256 1 1542 CRGAGAEPAANPRSPRSL	VPSLESTSTSVPPAPGTMATDSWALA
VDEQEAAAESLSNLHLKE	BEKIKPDTNGAVVKTNANAEKTDEEEK
EDRAAQSLLNKLIRSNLV	DNTNQVEVLQRDPNSPLYSVKSFEEL
RLKPQLLQGVYAMGFNRP	SKIQENALPLMLAEPPONLIAQSOSG
TGKTAAFVLAMLSQVEPA	MKYPQCLCLSPTYELALQTGKVIEQM
GKFYPELKLAYAVRGNKL	ERGQKISEQIVIGTPGTVLDWCSKLK
FIDPKKIKVFVLDEADVM	CATQGHQDQSIRIQRMLPRNCQMLLF
SATFEDSVWKFAQKVVPD	PNVIKLKREEETLDTIKQYYVLCSSR
DEKFQALCNLYGAITIAQ	AMIFCHTRKTASWLAAELSKEGHQVA
LLSGEMMVEQRAAVIERF	REGKEKVLV11NVCARGIDVEQVSVV
INFDLPVDKDGNPDNETY	LHRIGRTGRFGKRGLAVNUVDSKHSM
NILNRIQEHFNKKIERLD	
6257 210 615 AFIPAMAELIQKKLQGEV	EKYQQLQKDLSKSMSGRQKLBAQLTE
NNIVKEELALLDGSNVVF	KLLGPVLVKQELGEARATVGKRLDYI
	eqqretlaqlqqefcraqaakagapg
6258 210 615 AFTPAMARITORYLOGEN	
	BKYQQLQKDLSKSMSGRQKLEAQLTE
	KLLGPVLVKQELGEARATVGKRLDYI
TARIKRYESQLRDLERQSI	BOQRETLAQLQQEFQRAQAAXAGAPG
6259 2 1540 TLEKGEDSOCHDERKUKUT	
1 I I I I I I I I I I I I I I I I I I I	DDVLESSQENEDDHFWELLFHNNKTV
	VSLRNYPYKICDSCHMNLKNISGLII
	LLLDIRHEKIPIGEKSYKYDQKRNAI
	KNGQGFHDBAAFFTNKRSQIGETVCK
	RPHLEMEPYGCSICGKSFCMNLRFGH
	FCDNSAFIIHQGAYTRKILREYKVSD
	KSYDYNENGSNFSKKSHLTQLRRAHT
GERTFECGECGRTFWERS	NLTQHQRTHTGEKPYBCTECGKAFCQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	aequence	\=possible nucleotide insertion)
	Bequence		KPHLTNHORTHTGEKPYECKOCGKTFCVKSNLTEHORTHTGEKP
1			
			YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
1			IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECN
5260			ACGKTFSQRSVLTKHQRIHTRVKALSTS
5260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
1			RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
l .			RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPNI
1	1	1	VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
			SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEGEIEHHLAS
			NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCBIA
			OBIOEKLAIEAERRRIOEKKDEDIARLLOEKELOEEKKRKKHFP
			EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
ĺ	ľ		BIARKLOBEELLATOVDMRAAOVAODEEIARLLMAEEKKAYKKA
			KEREKSSLDKRKODPEWKPKTAKAANSKSKESDEPHHSKNERPA
			RPPPPIMTDGEDADYTHFTNOOSSTRHFSKSESSHKGFHYKH
6262	2	1759	PECHSQGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
5202	_	1,33	GSTRLVSQGLBALRSBHQAVLQSLSQTIECLQQGGHEEGLVHEK
1			ARQLRRSMENIELGLSEAGVMLALASHLSTVESEKQKLRAQVRR
			LCQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEFLGQLRQ
			YDEDGHTSEEKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA
1	í		
			AQQGGYETPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
			TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESIL
			GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
			NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
			PNVARTKNNLASCYLKQGKYAEAETLYKEILTRAHVQEFGSVDD
			DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
			NTTLRNLGALYRRQGKLEAAETLEECALRSRRQGTDPISQTKVA
Í			ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
			SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
			IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSPSPKP
			EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
			APVNTVMDSPVHLBPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
ľ	1	1	PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ
			DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ
			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
ŀ			IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
ì			SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
			AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ
	l		QSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKANTMA
			NQSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
	ſ		VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIOPYSSER
1			ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDBYVTFNGSYLL
			DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLOHSIE
			REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
1			PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRO
1			QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
1			VNDDFELTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
020.	443	1760	TOPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKG1
1			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
			SSTLVYNSMGTINOOAMDOLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTOGT
L			ADE VOTE FOR VWILKUPS DULKALGQP DI PURILEYS LKLTQGT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cystcine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T-Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SQKDKNFWLPRLCIRKFFPKKKCFVFDLPTHRRKLAQLEKLQDI
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLT
	1		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKV
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQ1
			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAII
			QTDQILTEKEKEIEVECVKARSAQASAKMVEEMQIKYQQMMEEN
		1	EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
		1	COGESTOLONEIOKLOKTLKKKTKRYMSHKLKI
6265	143	1960	KHROENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILGA
		ļ	TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	l	1	WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNONDSWIFTLAVLI
	l	1	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
	1		ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQG
	l	i	SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
	ł	ì	ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
	ì		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
		1	LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFOKKLAAOI
	[		DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
	ŀ	1	YCLFIQKLQDLEKKYYBEPRKGIQAEEILQTYLKSKESVIDAII
			QTDQILTEKEKEIEVECVKAESAQASAKNVEEMCIKYQQMMEEN
			EKSYOEHVKOLTEKMERERAOLLEEOEKTLTSKLOEOARVLKEE
		1	COGESTQLONEIOKLOKTLKKKTKRYMSHKLKI
5266	276	1421	GSHOKOMLVPCFLYSLONRKPSLYGSLTCCGIGLDGTPEVTAS
0200	2,0	1421	GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLE
			ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDF
	l	l	GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
			SINLGSPEOMPSEREVGTBAKNLLLAREDKKLOCLGLOSROLVE
		l .	LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIE
	j	ļ	RSGAPVLSLLSVRDGFIASOGDGSCFIVOODLDYVTELTGADCE
			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	
020/	,	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWE
			NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
			ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA
5050			VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1368	HRBLCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
			DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
			PNSDIPEREPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
		1	LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE
			SQANSGALDINQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
			KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
			IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
			GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
		1	SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATI
			TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
			GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
			FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
			IYPFWTPDIPLSSYVKGIYSFGLMETNFYDOAEKLAKRALSINP
		)	
		'	
		1	TDAWSVHTVAHIHEMKARIKOGLEFMOHSETLWKDSDMLACHNY WHWALYLIEKGEYRAALTIYDTHILPSLQANDAMLDVVDSCSML YRLOMEGYGYOGOWODVLDVARKHSRDHYLLFNDAHFIMASIGA
		*	

Deginning   Nucleotide   Carlamine, Cacystein   Contion   Continuo   Contion   Conti	tine, K=Lysine, ie, N=Asparagine, c, R=Azginine, v=Valine, ine, X=Unknown, *=Stop lectide deletion, insertion) SOSMAQROVFROLLHAALNCTS
Docation   Docation	Alalanino, Gedlycine, ilne, Kelygine, 10, MeAgparegine, 10, MeAgparegine, 10, MeAgparegine, 110, Xelbanown, *aStopeotic, 110, Xelbanown, *aStopeotic, 110, Xelbanown, *aStopeotic, 110, Xelbanown, *aStopeotic, 110, Xelbanown, *astopeotic, 110, Xelban
location   corresponding   c	ine, Kalysine,  10. MaBapatagine,  10. MaBapatagine,  10. MaBapatagine,  10. Walline,  10. Walline,  10. Walline,  10. Walline,  10. Malline,
corresponding to first amino acid amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence company. The company of the c	ne, M-Auparegine, , R-Arginine,
to first amino acid residue of residue of residue of residue of amino acid soguence sequence sequence sequence Soguence	, R-AXSININE,  "Valine, X-Unknown, *-Stop  Lectide deletion  INSERTION  INSER
omino acid residue of serine, T-Threonine, residue of amino acid sequence Serine, T-Threonine, w-Tryptophan, Y-Tyroz Godon, /-possible nucl condens acquance Bosphan, Y-Tyroz Godon, /-possible nucl condens acquance Bosphan, Y-Tyroz Godon, /-possible nucl condens acquance Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint sequence Bosphan, Y-Tyroz Godon, /-possible nucl condens acquaint se	V-Valine,  A-Unknown, *-Stopleotide deletion, insertion, insertion, SSNAGROVFROLLIHAALNOTS HITERLIHRAATVELMQ HEGEFONGEPAEIKITHEAYKKA TYMOGIGHLENGISSKESERT HTRLEILEKGLATELGNDLOEVF SAPOKAEVNONTSTESAGAVAA AABGHYTVSYOTDSGEFSSVOE LILIPMOGUTFIVNPAGEVSAFS
residue of amino acid sequence Codon, /possible mucl cold sequence Codon, /possible mucl cold sequence Codon, /possible mucl cold sequence Codon Sequence Codon Sequence Codon Sequence	ine, X-Unknown, *-Stop Leotide daleton, insextion) GUSHAQROVFKOLLIHAALNCTS **LTERLIKRATVHLMQ LEGEPONEPREIKITREAYKA **YKQIGHLHGISISKESERT TERLEILEKGLÄTSLONDLQBVE SAPOKLEVNONTSTSRAGAVA SAPOKLEVNONTSTSRAGAVA SAPOKLEVNONTSTSRAGAVE LILIPKGVIFTVNPAGEVSAPS
amino acid sequence Codon, /-possible nucl sequence Doppervielling mulcotide Codon, /-possible nucl Doppervielling nucleotide SVHKNYNAS LEMENDARPEPY NUCLEON SVHKNYNAS LEMENDARPEPY NUCLEON LUPPEPPERMCENLUS NUCLEON PASSISSOR PRASSICAN PRASSISSOR PRASSICAN PRASSISSOR PRASSICAN PRASS	leotide daletion, insextion, GSNAGRDVFNQLLIHAALNCTS LITERLIKRAATVELMG EEGPENGESPEERITITEAYKKA YMOGIOHLLBGISISSKESERT TTRLEILEKGLATSLQNDLQEVP SSPECHAEVNONTSITSAGAVAA JABGHYTVSYGTDSGEFSSVGE LILIPMGVGIFVNPAGEVSAFS
#squence \ \squancis \ \lambda coride  SOFFFORM LELLEF PREY LOCK  SVENION STATEMENT CONTROLLEF STATEMENT  6270 23 2086 SVIVITOS BORGEPTFHILES  FLYVIKICIANT DEL ACQUERAMN  GPOWESA ROMOÇKIKET LOCK  PASIS LOCK PROME PROPERT CONTROLLER  FASIS LOCK PROME PROPERT CONTROLLER  FASIS LOCK PROPERT CONTROLLER  FOR THE CONTROLLER OF THE PROPERTY CONTROLLER  FOR THE CONTROLLER OF THE PROPERTY CONTROLLER  FOR THE CONTROLLER OF THE PROPERTY CONTROLLER OF THE PROPE	inseytion)  KGSNAGRDYFNOLLIHAALNCTS  PLTERLIKKAATVHLMQ  HEQSPONGEPAEIKIIREAYKKA  YOGIGHLARGISISSKSSEHT  THRIEILEKGLATSLONDLOEVP  SAPOLAEVNONTSTPSAGAVAA  AABGHYVSSGTDSEEFSSVGE  JILIPNGVGIFFVNPAGEVSAFS  JILIPNGVGIFFVNPAGEVSAFS
DORPHOWLELLEFIRETYOUG 6270 23 2086 SVIVINGARELLEFIRETYOUG GEORGE PETITLES GEORGE PETITLES GEORGE PETITLES BERNELLEFIRETY BERNELLEFIRETY BERNELLEFIRETY BERNELLEFIRETY EFFRENCE PETITLES FOR SECOND SEC	GSANGROVFROLLIHAALNCTS PLTERLIRKAATVHLMQ HEGDFORGEPAEIRIIREAYKKA FYKOGIOHLIRGISISSKESSHT TRIBLIBKGLATSLONDLOEVP SAPQHAEVNONTSTSAGSAVAA AABOHTTVSYGTTDSGFSSVGE LILIPNGVQIFFVNPAGSVASP
6270 23 2086 SVIVINOSDORPPTHEES 6270 23 2086 SVIVINOSDORPPTHEES 6270 6070 SARAMON SARA	HLTERLIKKAATVELMQ HEQEPQNOEPAET KITAEAYKKA TYKQOIGHLERGISISSKESEHT KTRLEILEKKLATSLONDLOEVP SAPOHAEVMONTSTPSAGAVAA JAABGHYTVSYGTDSGEFSSVGE JILIPNGVQIFFVNPAGEVSAPS
6270 23 2086 SYVYTIGERORGEPTHIESE FLEVENGENTERIOLOGERANG GPOMESAROMOGNIKETIQNVE KLIPPEP FERMICELIEBERGEF PASILESEGGFEAEPAPTE EFYRMISGPFLETICIADDE YPOTHRUGELIEBUNDLIVURSE	MEQEPONGEPAETKITREAYKKA TYKOGIGHLLRGISISSKESEHT TTREETLEKGLATSLONDLOEVP SSAPOHAEVNGNTSTPSAGAVAA AABGHYTVSYGTDSGEFSSVGE JILIPNGVQIFFVNPAGEVSAPS
FLIVAKCIANTBELOQUEBANN GFOMBSARONQOKNETLIQVIS KLYPEFPENDICSKLEPROSF PASILSIPSOGPRAEPAPYTE EPYRNISOPPLETIJADOEL YEOYTRIVELINSLOVIJANS	TYKQGIGHLLRGISISSKESEHT TTRLEILEKGLATSLQNDLQEVP SAPQHAEVNGNTSTPSAGAVAA AAAEGHYTVSYGTDSGEFSSVGE JLLIPNGVQIFFVNPAGEVSAPS
GEOMESARONOGNIKETLONY KLYPEP PEKOMEGELDESOFF PASILSIPSOSCPAEAP PAYTEC EPYRNISG PP PLETICLIANDE YEO'RICHTREIDNSIDVUMSR	TRLEILEKGLATSLONDLOEVP SAPOHAEVNGNTSTPSAGAVAA AAEGHYTVSYGTDSGEFSSVGE JLIPNGVQIFFVNPAGEVSAPS
KLYPEPPKOMCEKLPERGYF PASLSLPSGSCPARAPATTPC EPYRNHSGPPLETLGLADERI YPGYLRIVRIDNSLDTVLNKR	SAPQHAEVNGNTSTPSAGAVAA AAEGHYTVSYGTDSGEFSSVGE LLIPNGVQIFFVNPAGEVSAPS
PASISLPSGGCPAEAPPAUTE EFYRNHSGPPFLETLGLDADEI YPGYLRIURSLDTULNE YPGYLRIURSLDTULNE	AAEGHYTVSYGTDSGEFSSVGE ILIPNGVQIFFVNPAGEVSAPS
EFYRNHSQPPPLETLGLDADEI YPGYLRIVRFLDNSLDTVLNRE	ILIPNGVQIFFVNPAGEVSAPS
YPGYLRIVRFIDNSLDTVLNRE	PGFLQVCDWLYPLVPDRSPVLK
CTAGAYMEPDTMLOAAGCEUGU	VLSSELPEDDRELFEDLLROMS
DERLOANWIRAKKEREPOTEGE	TRPSSDQLKEASGTDVKQLDQG
NKDVRHKGKRGKRAKDTSSERV	NLSHIVPCEPVPEEKPKELPEW
SEKVAHNILSGASWYSWGLVKG	ABITGKAIQKGASKLRERIQPE
EKPVEVS PAUTKOLV TAKOATO	GAAKVSQFLVDGVCTVANCVGK
ELA PHVKEHGSKT.VPEST.KKDV	DGKSPLDGAMVVAASSVQGFST
VWOGLECAAKCIVNNVSARTVO	TVRYKYGYNAGEATHHAVDSAV
NVGVTAYNINNIGIKAMVKKTA	TOTGHTLLEDYQIVDNSQRENO
EGAANVNVRGEKDEOTKEVKEA	
	GSCRLVBEEVNIPNRRVLVTGA
TGLLGRAVHKEFCONNWHAVGO	GFRRARPKFEQVNLLDSNAVHH
IIHDFQPHVIVHCAAERRPDVV	ENOPDAASQLNVDASGNLAKEA
	YREEDIPAPLNLYGKTKLDGEK
AVLENNLGAAVLRIPILYGEVE	KLEESAVTVMFDKVOFSNKSAN
MDHWQQRFPTHVKDVATVCROL	AEKRMLDPSIKGTFHWSGNEQM
TKYEMACAIADAFNLPSSHLRP	ITDSPVLGAQRPRNAQLDCSKL
ETLGIGQRTPFRIGIKESLWPF	LIDKRWROTVFH
6272 1136 528 GAVMEDAAAPGRTEGVLEROGA	PPAAGOGGALVELTPTPGGLAI.
VSPYHTHRAGDPLDLVALAEQV	QKADEFIRANATNKLTVIAECI
QHLQEQARKVLEDAHRDANLHH	VACNIVKKPGNIYYLYKRESGO
QYFSIISPKEWGTSCPHDFLGA	YKLQHDLSWTPYEDIEKQDAKI
SMNDTLLSQSVALPPCTEPNFQ	
6273 256 843 SCPRVSPECRSLGCQVMFSLPL	
SAAWNSKCHPGAGAAMARQHAR	
HVLIEDHRIVFSCKNADGVELY	NEIEFYAKVNSKDSQDKRSSRS
ITCFVRKWKEKVAWPRLTKEDI:	KPVWLSVDFDNWRDWEGDEEME
LAHVEHYAEVRDNTYCVLPT	
6274 56 1142 AAAMAAAAGGGAGAARSLSRF	
VDLTSVLRHVQSLEPDPGTPGS	
LAKEAFDEVDMAHRFAQEYKKD	PDRGYGAGVVTVFKKLLNPKCR
DVFEPARAQFNGKGSYGNGGAM	RVAGISLAYSSVQDVQKFARLS
AQLTHASSLGYNGAILQALAVH	LALQGESSSKHFLKQLLGHMED
LEGDAQSVLDARELGMEERPYS	SRLKKIGELLDQASVTREEVVS
ELGNGIAAFESVPTAIYCFLRC	MEPDPEIPSAFNSLQRTLIYSI
SLGGDTDTIATMAGAIAGAYYG	ADQVPESWQQSCEGYEETDILA
G275 20 565 SRRGRARGLARGSRRDVPRDAK	
	MAFMVKTMVGGQLKNLTGSLG
GGEDKGDGDKSAAEAQGMSREE	EEYQKQLVEEKMERDAÇFTQR
XAERATLRSHFRDKYRLPKNETI	JESQIQMAGGEVELPRELAKMI
EEDTBEEEKASVLGQLASLPGI KCHVM	MINISTER DE L'ALIANTE DE L'ALIA
6276 797 97 TELPEPEPEPEPERILENTGER	TO THE PORT OF THE
SCLQQLATHPGHWGIHLQIAEP	MURESLALLAKUSSLGLUMP
VWVGAKISHGSFSVPGHVAGREI	MCCONCANT CUICES OF THE
LGSGYRRQLLTDMLELCQGLWQI LASSPRATVTVEHNPAGGDYASV	TOTAL TANDALONS TAGALGRE
GYHKDLLAHVGRN	WIMPINGANANCE TRANSFER
GIRKULIAHVGKN	

SEQ Predicted Predicted and Nation acid segment containing signal p ID beginning nucleotide (As-Alanine, C-Gyoteine, DaAspartic Acid nucleotide location Courseponding (Hellicitidine, I-Isoloucine, Krygline,	d. E=
NO: mucleotide location Glutamic Acid, F-Phenylalanine, G-Glyc location corresponding H-Histidine, I-Isoleucine, K-Lysine.	ino
Location   corresponding   H=Histidine, I=Isoleucine, K=Lysine.	
	,
corresponding to first L=Leucine, M=Methionine, N=Asnaragine	
to first amino acid P=Proline, Q=Glutamine, R=Arginine,	
amino acid residue of S=Serine, T=Threonine, V=Valine.	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown, *:	-Stop
amino acid sequence Codon, /=possible nucleotide deletion.	
sequence \mpossible nucleotide insertion)	
6277 4600 2744 MAFRIENGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEY	PLVINT
LKRFNLYPBVILASWYRIYTKIMDLIGIQTKICWTVTTC	BEGLSP
TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSG	RLGGL
VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLV:	HILRA
TKLYRGSLIALCISNVFFMLFWQFAQFVLLTQIASLFAV	TYVVGY
IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSI	VIIWG
ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSI	KIFGIA
NDAHIGNLLTSKFFSYKDFDTLLYTCAABFDFMEKETPI	RYTKT
LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDH	GELVY
HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLH	GWLFC
KVHPGAIVPAILAAMSIQGSANLQTQWNIVGEPSNLPQE	ELIEW
IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAC	LRART
KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSH	CPGCSM
PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVY) KE	CAPEAA
6278 3 823 ILFRLVLLSLVYLLNSVATEERKPABVLIVEGOOYAVVG	mi ve s e
IRILEYCQQVDNIPSVTTDMLTRLSDLLKYFNSRSCQI	TVLLL
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RSCHAPTIDLAAHBUKVISVDWIDTGLLLSGGADNKLYSYRYSP				ASCRAF DI DUMANDURVES VEWTOTGELES GGADNKEYSYRYSP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
CN:	beginning nucleotide	nucleotide location	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	seddence		\=possible nucleotide insertion)
6287	2.78	1482	TTSHVGA
0207	2/0	1482	MQFFFNFQIGLRSTSGKEKYSGDAGFLGDALCLFLQCLALDEDF
			APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
			MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
			NKLKKQGETPNEVCMFSLAYGDIPEBLIDVSDFBCSLCMRLFFE
			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
	1 .		QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA
	,		YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY
			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
6288	1	743	YLEDV
	1 -	/63	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
	1		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
	l .		HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
	ì		KVGLAIKPGTSVEYLAPWANQIDHALVMTVEPGFGGQKFHEDHM
			PKVHNLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6289	1	743	RSEDPRSVINLLENVCSEARQERSLDR
0203	1	74.3	VTLYPCRGLVGNLLLGASSMASGCKIGPSILNSDLANLGAECLR
			MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
			PKVHNLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6290	3	1856	RSEDPRSVINLLRNVCSEAAQKRSLDR
0230	,	1929	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRRMISRYTRKA
			VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
			DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
	i .		QNATEKVÇTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
			RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
			GKKLHFSSSYAHKASSIAKSSSFCSMERDREDSIIVSEGIIEEY
			LAFDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
			VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESECV
			LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
			TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
	i		RVPVAPDSLSSPSFTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
			PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
			QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P
6291	1732	602	
		602	LVAKMASSASARTPAGKRVINGEBLRRLMKEKQRLSTSRKRIES
			PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG
			AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST
			SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEGD
			GERKRGDASKPLSDAGGKEHSVSSSREVTSSVLPNDFFSTNPPK
			APTIPHSGSTEKAETHEKVVKRRENTARALPEGFFDDPEVDARV
			RKVDAPKDQMDKEWDEFQKAMRQVWTISEAIVAEEDEEGRLDRQ
- 1			IGEIDEQIECYRRVEKLRNRQDBIKNKLKEILTIKELQKKEEEN
6292	1835		ADSDDEGELQDLLSQDWRVKGALL
0232	1932	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLINAVV
- 1	- 1		LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
- 1	!		LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
- 1			SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
			LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
- 1			AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
6293	2382	1035	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1 1		1	MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK
1 1			LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY
1	,		HASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA
			APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRL
1 1			LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP
1 1			ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDD
[ [		1	PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
6294			NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
1 1			KNVIATASDYDMAEITNIRPSFDVSFVVAGLIGASVLVVCVSVT
]			VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKTTK
1 1			VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
1			LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
1			DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
1			VKTRVLRKTLDPVFDETFTFYGiPYSQLQDLVLHFLVLSFDRFS
			RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
1 1			SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
1			RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
i I			RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
6295	2795		EY
0293	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
1 1			TRRLSSSESPORDPPPPPPPPPPLLRLPLPPPPQQRPRLQEETEAA
1 1			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS
1			TIESGYGEAPPPTESLEALPTPEASGGSLEIDFQVVQSSSFGGE
			GALETCSAVGWAPQRLVD7KSKEEAIIIVEDEDEDERESMRSSR
ł I			RRRRRRRKQRKVKRESRERNABRMESILQALEDIQLDLEAVNI
			KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
1 1			ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT
1 1			NMVIVKEFQRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHS
1 1			FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK
			QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK
1 1			ISDFMETTDYFETTDNBITDINENICDSENPDHNEVPNNBTTDN
1			NESADDHRTTONNESADDHNENPEDNNKNTDDNEENPNNNENTY
			GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
			SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
1 1			SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS
6296	727	1199	DLEDVLQVPNGWANPGKRGKTG
	/	1177	RHCGCDAQGACDSLPPTGTSSPVTARNALPEARCCVWLLDGTTV
	1	ļ	EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTERDT
	i		LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
6297	1	922	KWALIHKRVRLSVFGARWGRIYFGK
	*	764	QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
	i		VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII
	I	i	VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN
	ľ	1	NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL
. 1	I		MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
			FUNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ
6298	3	985	GARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGQRSTM
	,	303	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
- 1	1	1	PFGPHRGLSVLLARIPQRAPRWLPACRQKTSLSFLNRPDLPNLA
- 1		1	YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
		1	YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
			WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLFVELKKEVEM
		1	KGVWSMPSKYSEBGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
			RGYMSMPSKYSEBGYYNVQYSFIKEAEHHCLLHSFIPYNCFIRL LHGMKDDIYDWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI QLLVYTIDDLIDKLSTIVN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleuc_ne, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6299	512	814	BCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
			SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
			NKEEEVQLRNNH
6300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWCAWRQGARA
1		ł	AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR
1			LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
1			ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
			WFEVNRSCPEHPSD
6301	616	284	GKFVPVNWEPPQPLPFPKYLRCYRCLLETKBLGCLLGSDICLTP
			AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
		ĺ.,	IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDFC_LLS
			PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWQSWQEKHPGQALSSEPWNFPDTKEEWEQHYSQL
1			YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
			KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
			QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS
			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
			PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
			HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
			SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
			DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV
			PDEQDCVTQEVPDSRQAETEAEVKKKKKKKKKKKKVNGLPPEIAA
			VPELAKYWACRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
			VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDFVKIALA
1			RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLEPPWGGPDYA
			TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
			LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE
			DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
1			WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
1			WPGSVEKLQGSVWCDAETLLSSSRTGGQAFFWLTDHDVQMLRLL
			AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL
1			CGLIKRFGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
			TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN
i i			WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
			PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
1			EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE
			SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
6305	99	420	NMIWKGRSTYRPRPRRSVPPPBLIGFMLEPGDEEPQQEEPPTES
			RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
			VQGKILTKSEQFKMPEGR
6306	1	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
1			KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
)			ESEDSGVIPGSHSENALHASKKEGEGGGKAQSSLGYIPLMRVVQ
1 1			SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFO
			NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
			TYFVGEMPGGTPGGPSGQGABAARGWETAIRQALMPVILQDAPS
1 1			APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGOF
1 1	i		GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
1 1	1	1	HPGIVNLECMFETPERVFVVMEKLHGDMLEMILSSEKGRLPERL
i 1			TKFLITQ1LVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC
1			DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
		ļ	VIMYVSLSGTFPFNRDEDINDQIQNAAFNYPASPWSFISAGAID
		ļ	LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER
1 1			YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG
			District of the state of the st

SEED				
Degining   mucleotide   Cocation   Callanine, C-Cysteine, DaAppartic Acid, Etc.	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding   Coffee   Contemporary   Coffee   Contemporary   Coffee   Contemporary   Coffee   Contemporary   Coffee   Contemporary   Con				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Contemporary	NO:			Glutamic Acid, F-Phenylalanine, G-Glycine.
to first amino acid acid acid acid acid acid acid acid				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of mino acid anino acid sequence of sestine, Twithconine, Vavaline, acide of quence of mino acid anino acid sequence of codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide incertion)  LARRISTVI.  CHILIPRENDE PEPRABARAPCAPDA PUMSPER VVRCSKFENVED ON POSSIBLE ON POSSIB				L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid amino acid amino acid amino acid acquence (acon, "possible nucleotide deletion) (acon, "possible nucleotide deletion) (acon, "possible nucleotide deletion) (acon, "possible nucleotide inserti	1			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence				S=Serine, T=Threonine, V=Valine,
Soquence	1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6310  2136  569  CPLIPAGIOP PEPERGRAPPOR PRINTPRIVIPE CONTRIBUTION OF THE PROPERTY OF THE PROP			sequence	Codon, /=possible nucleotide deletion,
5897  2136  589  CILLIPAGENDE PEPERAMANPAGENDE MYSTER VITYGESTEPHINYON OPPENDING THE SOCIAL VEPLANCE AND AND AND AND AND AND AND AND AND AND		sequence		\=possible nucleotide insertion)
OPVINIOCITEDITA/SPOWLE/PUCAL/NEWIAL/TVE/SAGGRADI  VILPISSTERIER TRANSPYTOCHTOPOLITOR/DINOR/TAGGRADI  VILPISSTERIER TRANSPYTOCHTOPOLITOR/DINOR/TAGGRADI  SAGCOMVAI INVENDEZAER/TAGGRADIPOLITOR/DINOR/TAGGRADI  GENERAL/TAGARDO PRINCESSAGA SILEPIDI TAYS YANGO TAGADON PET OF SAGCOM TO PROPERTY OF SHARING A PROPERT				
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TOWNQTERIOLISPLITEWVILESITERIOLISPLATIVISES LIPELITYSWINESISPLES SAGGMONTH INFORMATION SHIPPLATIVISES PLANT SAGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH INFORMATION SHIPPLATIVISES AGGMONTH SHIPPLATION SHIPPLATIVISES AGGMONTH SHIPPLATIVISES AGGMO	1			QPVKNDQCYEDIRVSRVTWDSTYCAVNPKFLAVIVEASGGGAFL
SAGCONVULINNOSTABELYRLDSLIPPLITYTVSNINNOSISJECS ARCHESVEL I DERROTTLVARERHARGARPHER I FLADRICKTETT GESNISERGLANDERHERGANDAGELDSSNOALLEPTOPTOTS VYCKORGOSS I TRESTIERPTYTI JATPTYSERE GERMONSIPPE GESNISERGLANDERHERGEN LIGHT I JATPTYSERE GERMONSIPPE GERMANDER HER LIGHT FRANKERSE I WIT VERTEN GERMONSIPPE GERMANDER SILLAR PASTTABLAT PROSIDENCIA GERMONISER GERMANDER SILLAR PASTTABLAT PROSIDENCIA GERMONISER GERMANDER SILLAR PASTTABLAT PROSIDENCIA GERMONISER GERMANDER SILLAR PASTTABLAT PROSIDENCIA GERMONISER GERMANDER SILLAR PASTTABLAT PROSIDENCIA GERMONISER GERMANDES SILLAR PASTTABLAT PROSIDENCIA GERMONISER GERMANDES SILLAR PASTTABLAT PROSIDENCIA GERMONISER HER PAST PROALDELLY CYCOSINUL PET PATALON OF MENER I TILLAR GERMONISTORI LA	i			VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
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GSSMSERGLALADPENLESHALQELISSINGALLEPTYDPTOTS VVIVORIGOSS, TYPETITED PTYLIPTYTS REGIONASSAPRA GLEVSKELTAFYKLIERKECE! VWIVORRISSIFORDOLYPOTAG PERALSBERUNG STREET INTERTYTE INTERTYTE SERVENS GEBAALBRUVESGORD I LIEUTAFYKLIERKESHOOD OR FOR STREET GEBALBRUVESGORD I LIEUTAFYKLIERKESHOOD OR FOR STREET GEBALBRUVESGORD I CHEROLIERKESHOOD OR FOR STREET GEBALBRUVESGORD I CHEROLIERKESHOOD OR FOR STREET VARIOUND VERHOROUT VYTESKOD OR GEBAUTURS I LIEUTAFYKLIERKEN STREET	l.			SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
VYVOKGOSSI RYPETIEEPPYIHEANTPISEEDGKMOSMYERG GLEVISCELLARYKLHERKEET UNIVVERSEIDIGDOOL POPTAG GLEVISCELLARYKLHERKEET UNIVVERSEIDIGDOOL POPTAG FRAALMERWISGRAD PLISIAEAAVUREKGELKIET SKRIVUS GELAALARUKVOORDI CLEISOGLARINGKOO GELAALARUKVOORDI CLEISOGLARINGKOO GELAALARUKVOORDI CLEISOGLARINGKOO GELAALARUKVOORDI CLEISOGLARINGKOO GELAALARUKVOORDI CLEISOGLARINGKOO GELAALARUKVOORDI CLEISOGLARINGKOO HENRERI I YLANKOS ORDI CLEISOGLARINGKOORDI CLEISOGLARINGKOO HENRERI I YLANKOS ORDI CLEISOOLARUKUVUTPEI KARTH  KIHHI DI ONIVERSEI CHEKOORDI CLEISOOLARUKUVUTPEI KARTH  KIHHI DI ONIVERSEI KIKTUPENLI LIBOOLARUKUVUTPEI KARTH  KIHHI DI ONIVERSEI KIKTUPENLI LIBOOLARUKUVUTPEI KARTH  KIHHI DI ONIVERSEI KIKTUPENLI LIBOOLARUKUVUTPEI KARTH  KIHHI DI ONIVERSEI KIKTUPENLI LIBOOLARUKUVUTPEI KARTH  KONIVERSEI KORVOORDI KORKOORDI KORKOORDI KORKOORDI KORKOORDI CORKOORDI  GERVAKURUKUPE CORKOORDI CORKOORDI CORKOORDI CORKOORDI CORKOORDI  GERVAKURUKUPE CORKOORDI CORKOORDI CORKOORDI CORKOORDI CORKOORDI  GERVAKURUKUPE CORKOORDI CORKOORDI CORKOORDI CORKOORDI CORKOORDI  GERVAKURUKUPE CORKOORDI CORKOORDI CORKOORDI CORKOORDI CORKOORDI  GERVAKURUKUPE CORKOORDI COR	1			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
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PRAMABABENINGRADAP LISTARATYPENGRADANS SIRRANIAS BERMANIAS SILIGAPASTITARATYPENGRADANS SIRRANIAS BERMANIAS SILIGAPASTITARATYPENGRADANS SIRRANIAS GERMANIAS SILIGAPASTITARATYPENGRADANS SIRRANIAS GERMANIAS SILIGAPASTITARATYPENGRADANS SIRRANIAS GERMANIAS SILIGAPASTITARATYPEN VIGINIA SILIGAPASTITARATY URSPERIAS SILIGAPASTITARATYPEN VIGINIAS VILIGAPITALIAS UNDA SILIGAPASTITARATYPEN VILIGAPAS VILIGAPITA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPASTITARATYPEN VILIGAPASTICA SILIGAPA	1			VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
BSRPMANGSSILGAPASTTTANATPOSGIARAGEGILAGENCILAEW   6308   2	1			GLEVSKCEIARFYKLHERKCEFIVMTVPRKSDLFQDDLYPDTAG
BSRPMANGSSILGAPASTTTANATPOSGIARAGEGILAGENCILAEW   6308   2	1			PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
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VPILLILAGNY/NVOALROSPOQODBER/DUFPY/SMASS/SPOQI WOGNVUAL KESSKSORMEN/NVFILESPOTMONICAG/LONDI GRADARITAFILOSSY/SOUPHINESPOTMONICAG/LONDI BERKANICAGI LONGSSY/VOOPHINESPOTMONICAGE/PY/VVPRDI_GVV BERKANICAGI LONGSSY/VOOPHINESPOTMONICAGE/PY/VVPRDI_GVV BERKANICAGI LONGSSY/VOOPHINESPOTMONICAGE/PY/V/PVPRDI_GVV FLOMESIALAGURVENSSAN_DESTYTTO/GGAZAGI LARCTSIV/T TESLISSASSPPVEITWITSADTIEVEDRISTETILESVASAGO/SVV YTOSTOSSDSSALALILADTISTSY/MOGRAMORISSO(SSSPPYSK YTOSTOSSDSSALALILADTISTSY/MOGRAMORISSO(SSSPPYSK	1			IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
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FLOMLBAIKALEVENKENABALEENTTOKREAKKAKIAETSNYI TESLPSAESEPVEIRVEIAEGTIEVEEDGIEFILEEVASAKSVK YIOSTGSSDDSALALLADITSKYRGGPRKGQIKEJGCPSDPTSK	( )	, 1		
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		1		
QVEGIEIVKLQLSHVKDLFHCEKCNRSFKLFYHFXEHMKSHSTE	1 1			
	-			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid .	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
1			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
1			LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
1			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVO
1			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
1			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELEVERVNQ
1			MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
			AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFWPLGVL
1			FHRRRANGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
			RLNEQREQUEFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
			TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
			FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
			TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKOSVK
			YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCPSDPTSK
			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
1			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
i			LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
1			PNHCTLCDLWFMOGNELRRHLSDAHNISERLVTEEVLSVETRVO
			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNO
			MPVEVQTELLEADLDHVTPEIMNGEERESSGADAARAAREDHED
			AEDLETKPTVDSEAEKAENEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATREAPYWTYLLCALGLFTYQSLDA
1			IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY
			PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVT3IOIALVI
			VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF
			HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
			VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP
			GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLOISRH
			LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFRADENENITVVKGIRLSENVIDR
1			MKESSPSGSKSORYSGAYGASVSDEBLKRRVAEELALEOAKKES
1			EDOKRLKQAKELDRERAAANEOLTRAILRERI CSEEERAKAKHL
1			ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
i			EBVEAKFKRYESHPVCADLQAKILQCYRENTHCTLKCSALATOY
1			MHCVNHAKQSMLEKGG
6317	102	839	PEAGTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
1	l i		FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
1			TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
	l l		<b>EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG</b>
ĺ			QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
			PAITAAKONTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAKGREGADSMSHLPGLELRREAPPL
1			LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
			LAPVRRDRVLABLPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
	1		VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
1			ERFEVLGIPFSLOLWDTAGOERFKCIASTYYRGACATIIVFNLN
1			DVASLEHTKOWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
1			EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFRANVLA
	· I		BLEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
	! I		
6319	88	717	
6319	88	717	AATMRINONTLILIGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT
6319	88	717	AATMRLNONTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLBQEYAMQCSWOBDADKCTFIVLDAEKWQAQPGATEES
6319	38	717	AATMRINONTLILIGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
			TLRLTVSESEHQWLLBQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
ł	1		RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
			IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			EDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
			PTPQLAAFSASKAYLDHFSRALQYEYASKGIPVQSLIPFYVATS
1	1	[	MTAPSNFLHRCSNLVPSPKVYAHHAVSTLGISKRTIGYWSHSIQ
			FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
			RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
1			VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
1			FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1	ĺ		NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
l			IPGGMVDPGEKISATLKREFGEEALNSLQKTSAEKREIEEKLHK
			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
1			LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
6322	5045		EADCHAL
6322	2047	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
			WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
1			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
1			RYDDIENFPLSELMTEISTGVETTANSSISLRSTTLEKEVPVIF
1			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
1			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
6323	1.	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALOA
0323		556	PASTTDGAGEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
1			EKKIMINPITVIEVYPDITEVNDYYLWSIFNFVYLNFCCLGFIA
			LAYSLKVRDKKLINDINGAVEDAKTDRLINITRSGLAASCIMLW
			MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMERCPCEGSLNEAEAGALPAARMGLEAPEGGEREOPGO2
	-	2002	RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
1			PQAEFWTDGQTEPAAAGLGVETERPKQXTEPDRSSLRTHLENSW
1			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPWTOPGVHGP
			WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
i .			PSADGSWKELYTDGSRTQODIEGPWTEPYTDGSOKKODTEAARK
			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
1			EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAOPVGPPS
1			RVEGGSGGFSSASSFDBSEDDVVAGGGGASDPEDRSGSKPWKKL
1			KTVLKYSPFVVSFRKHYPWVOLSGHAGNFOAGEDGRILKRFCOC
1			EQRSLEQLMKDPLRPFVPAYYGNVLQDGQTFNQMEDLLADFEGP
1			SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
			EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNF
1			KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
			KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPOVKMSNYVNDMWPGSPOEKDSPSTSRSGGS
1			SRLSSRSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRSRRRHQ
1			RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
			RSRSRGRSYCGRAYALARGQRYYGFGRTVYPEEHSRWRDRSR
			TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFÇKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGH_YVLMGLLPPPWTISFT
	ſ		VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA

Seg				
Note				
Corresponding   Coffeet   Corresponding   Coffeet   Corresponding   Coffeet   Comment   Corresponding   Coffeet   Comment				
corresponding to first amino acid residue of samino acid residue of samino acid residue of samino acid residue of samino acid sequence Sessine, T-Threonine, V-Valine, P-PROSINE, Geditamine, R-Arginine, S-Sesrine, T-Threonine, V-Valine, M-Tryptophon, V-Tr	NO:			
to first amino acid am				
######################################				L=Leucine, M=Methionine, N=Asparagine,
xeadue of amino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid asquence (Codon, 1-possible nucleotide datein)  6327 1 1 1337 SLATIATE PROPERTIES IN INSTANCE AND ANASYOGENESSES (CODON, 1-possible nucleotide insertion)  8 SLATIATE PROPERTIES IN INSERTIES AND ANASYOGENESSES (CODON, 1-possible nucleotide insertion)  8 SLATIATE PROPERTIES IN INSERTIES AND ANASYOGENESSES ANASYOGENESSES AND ANASYOGEN	1			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence  Codon, /-possible nucleotide diaction, -/possible nucleotide insertion)  SAMPHONE STATEMENT (SAMPHONE)  SIGNAL PROPERTY (SAMPHONE)  SIGNAL PROPERTY (SAMPHONE)  SIGNAL PROPERTY (SAMPHONE)  LINATEN AND AND AND AND AND AND AND AND AND AN	1			S=Serine, T=Threonine, V=Valina,
Sequence   \  \  \  \  \  \  \  \  \  \  \  \  \	1			
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6327 1 1337 SLAFILLER GOSVWETTOOTANET FERTPERSELS GULLETS NO BOSGONKAL PEPOPOAR GENER TESKLOLAREK KORKGESTEEK GARRETOSAV SARQOOPTEELDE SSI OLGTTER KYTHOGRSCHAE LARER KORKEN FERNOL FERT SKEN SARQOOPTEELDE SSI OLGTTER KYTHOGRSCHAE LARER KORKEN FERT SKEN SARQOOPTEELDE SSI OLGTTER KYTHOGRSCHAE LARER KORKELT SKEN SKEN SKEN SKEN SKEN SKEN SKEN SKEN		sequence		
DISSONMABILEPOPORANGEMENTERIOLOLARESCONCRETERIO GRAPPTOSANA SANQCOPPERED SSOI GLOTTERIVAGRISMA LIMARRANGGERALIGANISMO GOOPPERASSESTAGETHOOVIRG LIMARRANGGERALIGANISMO GOOPPERASSESTAGETHOOVIRG LIMARRANGGERALIGANISMO GOOPPERASSESTAGETHOOVIRG ROMAINTONISMO SANGCOPPERASSESTAGETHOOVIRG ALGORITOTE PROVINCIA THE PROVINCIA SANGCOPPERASSESTAGETHOOVIRG RANGCOPPERASSESTAGETHOOVIRGO SANGCOPPERASSESTAGETHOOVIRG REPULSORITONISMO SANGCOPPERASSESTAGETHOOVIRGO SANGCOPPERASSESTAGETHOOVIRGANISMO S				
GARPTOSAVSAQCOGPTERLESSI OLOTPERTUPAGRISAS  LARSTRANGERALKQANKEN GOOPPTERSESSI OLOTPERTUPAGRISAS  LARSTRANGERALKQANKEN GOOPPTERSTEER GETPEOTYRE  LEBTTOVEDELLERILVEKREROOVPTERKTOGRIVGEK SEITSHLOTES  ROMALTOTETPENBELSSI LANDELGY SOOLINGER GETPEOTYRE  ALGOVI TOPTTPENBELSSI LANDELGY SOOLINGER GETPEOTYRE  ALGOVI TOPTTPENBELSSI LANDELGY SOOLINGER GETPEOTYRE  ALGOVI TOPTTPENBELSSI LANDELGY SOOLINGER GETPEOTYRE  ALGOVI TOPTTPENBELSSI LANDELGY SOOLINGER GETPEOTYRE  SERVANGER SOON HILL VERSEN SOOLINGER GETPEOTYRE SOOLINGER  SERVANGER SOON HILL VERSEN SOOLINGER GETPEOTYRE GETPEOTYRE GETPEOTYRE SOOLINGER GETPEOTYRE GETPEOT	6327	1	1337	
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LDETPLYVEDLLIGRIUMSKERERGYVETROTOGRIVGI.FSHI.HOYS RONGLIOTER ESWITERAMULGI.SVOGLINGSRICIALIR ALCONJONYTENBELSSDLVHILLEYMISTICCEP.SSADBUR ALKEIMER ITS USVISKRERERGISERAL REVVEETRIGHT BERNALDINGSRICH STANSKERERGISERAL TREVVEETRIGHT GERMAN STANSKERERGISERAL TREVVEETRIGHT BERNALDINGSRICH STANSKERERGISERAL TREVVEETRIGHT GERMAN STANSKERERGISERAL TREVVEETRIGHT GERMAN STANSKERERGISERAL TREVVEETRIGHT BERNALDINGSRICH STANSKERERGISERAL TREVVETRIGHT KATLEV ILRE KIGLEVIARKSERELIERI TERAVILOTISPERGISER KATLEV ILRE KIGLEVIARKSERELIERI TERAVILOTISPERGISER KATLEV ILRE KIGLEVIARKSERELIERI TERAVILOTISPERGIS TVILOVYSISKERRARVILTFALDSVERKLIMSSTEGITSPIT VILOVYSISKERRARVILTFALDSVERKLIMSSTEGITSPIT VILOVYSISKERBANDALISPERGISERAL TREVTERAVULGTILIPERGIS SERTILOTISPERGISERARVILTFALDSVERKLIMSSTEGITSPIT SERJAMOOFFINANSE VILOVERSE SERVILOMSSTEGITSPIT SERJAMOOFFINANSE VILOVERSE SERVILOMSSTEGITSPIT SERJAMOOFFINANSE VILOVERSE SERVILOMSSTEGITSPIT SERVILOPSTEGITSPIT SERVILONSKALLATISPIT SERVILOMSSTEGITSPIT SERVILOPSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOPSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOPSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOPSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOMSSTEGITSPIT SERVILOPSTEGITSPIT SERVILOMSSTEGIT SERVILOMSSTEGIT SERVILOMSSTEGITSPIT SERVILOMSSTEGIT SERVILOMSSTEGIT SERVILOMSSTEGIT SERVILOMSSTEGIT SERVILOMS				GARPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
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TYESCLIN  3 495 QOGGWITTGRERACNSATT LEGGUDLSYPETHALLKVAGWYLL LLAF LOVESSLATMYSASYSFEVYT KOOLINLLAFYLWALEFRY RWLTCISWILSELEHLINLTLALLASVAGWSTELVALLSTVAGE FRUTCISWILSELEHLINLTLALLASVAGWSTELVALLSTVAGE FRUTCISWILSELVAGE FULLEREN YSBOYLWAGE TEWTLVALLSTVED  WITSSINGEDUNGST FULLEREN YSBOYLWAGE TEWTLVLESVEDI NLIDYLBFILLDGIPOLLOGIGGRES IRWNSEVYLOSFELEE KENNES SVENDAGMAIL IN THEOTOTOLOGIC JURKOWEEF FOR ARWELEY EUROPOGRAFT FULLEN OF GETTAGE SOURCE FULLEREN UNGALERHLAND OF FUNDAMEN FOR FULLER TENDEL VIGWALERHLAND OF FOR THE TOTAGE SOURCE FOR THE TOTAGE SOU	1			
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RVLTCTSWILSELIAHILOTLIALIASIVARSKYNDSGLVAGA 1 PORMOFFICARSKYNS VISITSCYCTOSTOAN 6332 1 878 VTESRNFEDLVSFTPLIERERIYSROYAGOFIGHIULIGSVFDI NILDVILBELLOLOFOLIODORGERIKOMEVOLOFFIGHIULIGSVFDI SVERARMANILVIHCOTTODLIQUIAMCMMEETIQLAGEVALLEY SSGILTAVLPCLATIORIKSIERERIMCTWOLOFFICARDVALLEY SSGILTAVLPCLATIORIKSIERERIMCTWOLOFFICARDVALLEY USGALLEPHALOROFOLIORISCHE SIELALIISCHOPERDO VIGWALIPHILANDROSSGORPSIELALITSCHOPERDO VIGWALIPHILANDROSSGORPSIELATERIALITSCHOPERDO LUSTWARTIGOLVETOTILEPROAVSSSI 6333 3 1467 RTPSSEARGORSPGCVSALISPYRARDVSLAPLITPERSAG OPLTFSPGGROPERSLLVMCMSGGGRRSSISPYRRFGTGARRS GLAMMGROPHITAMMEHTMOGRAGAMEVPUPEDMEMPGMORPHOGOP	5331		495	
1 INGPANCEL CHASTAIN SYKISCUTQSTDABY 1 878 VITESINGEDUS PETLELERIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELERIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELERIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLERIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLELIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESINGEDUS PETLENIK YSBOYDAGO YI TUSHISTOFIN VITESIN				
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SUKPABRANILVIKOOTTODLOQLAMCKMREFIOLAGEVALLEY SSGILTANLPGLATIORKEN ELEVANVANOSMEKKUTYPEDDELD ELEPGGROAFFIDDIALEKOROTASGET FEILLISGCOPEPD USGVALIPHIKANDVANOVATTUATORGOSSGOPPEGGOTO KLSTWATIGOLVETGTGLEPRGAVSSSI  6333 3 1467 TRIPSSEARGOSSPGGVSABAIDVTAGREVSILAPLITFESRAG OPLITSIPSGROPURSLIVANCHSGGGRRASSISPINHEGTGARRS GLAMGROPURTAMMEHIMOGROAFFUPOHEMOFINGGEP	6.5.52	1	878	
SSGITTAVLPCLATURKKSIKEVANY-NOSLMKIVTPENDGLID ERREGGORAFTEPDDAL PROGRESSGSFTEHLISTSCHPENDGL VIGVALUPHLSNGOVPNYVPTTIVAATORSOSSGSPPECLOTIO KLSTWARISGLVKTGTGLEPRANYSSSI  6333 3 1467 TRIPSBARGOSSFTESKSSTSSTSTSTRFTGTGARRS GPLTTSPBARGOSFTGSTGSARISDWTAGRFVSLLAPLIPPRSAG OPLTTSPBARGOFTRSLLVMXCSGGGRRSSLSPVRRGTGARRS GLANGRIGHERHAMMEHPMOGRAGENPOFTPOHERMOFTMOGRF	1			
ELBPGGROARFTPDDALKPGGTASGGTTFSLALLTSCHOPEPSD UTGVALGPHLENDUTVTCTGLEPRGAVSSST  6333 3 1467 ETTSSEARGASSPG-GSARJASVTAGKTSLAPLTFFSRAG OPLTFSPGGROFFDGFTAGKTSLAPLTFFFSRAG OPLTFSPGGROFFDGFTAGKTSLAPLTFFFSRAG OPLTFSPGGROFFDGFTAGKTSLAPLTFFFGGRAFS GRANGEFGCHTAMMEHTPGGGARGANDFPFEGMGWFGGFTAGKTSLAPLTFFGGRAFS	1			
VIGWALEPHLSMOZYMYVTFTTVAATORGOSGSSPPCEQOTO KLSYMATISQUVTOTGLEPRQAVSSSI  6333 3 1467 TRYPSRAEAGGSSPCSCVSAHISDWYTACKPVSLLAPLIPFRSAG QPLTYSPSGRQPLRSLLVGWCSGSGRRSSSISPYRKTGTGARRSI GLANGRIGHERHARMEHPWGGSGRRSSSISPYRKTGTGARRSI GLANGRIGHERHARMEHPWGGSGRRAWPDVPERMSUFFDWGFWGGFP	1			
LUSTWATISQLVETTOTILEPRQAVSSSI   S133   1467   THTPSEABGORPGCVSATSDPTAREFVSILAPILTPERSO OPLITS PSGROPLESLLVEMMSGGGRRASSIS PYREFGTGARES     GLAMGGFGHHTAMMEHIMOGGGRASSIS PYREFGTGARES     GLAMGGFGHHTAMMEHIMOGGGRASSIS PYREFGTGARES	1			
6333 3 1467 TRIPSEARAGGESPG-CVSAHSDWTAGKEVISLLAPLIPERSAG QPLIFS PSGRQPLRSLLYGMCSGGERKESSET PYREGTGARG GLRWGHPGMHYAPPWGQPANDPPVPHGMMECOMMPRIGGEP	1			
QPLTFS PSGRQPLRSLLVGMCSGSGRRSSIS PTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGNMPQMMPPMGGPP				
GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPPMGGPP	6333	3	1467	
MGQMPGMMSSVMPGMMMSHMSQASMOPALPPGVNSMDVAAGTAS				
	L			MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	location	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	to first	to first	L-Leucine, M-Methionine, N-Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
	sequence		GAKSMWTEHKSPDGRTYYYNTETKOSTWEKPDDLKTPAEOLLSK
			CPWKEYKSDSGKPYYYNSQTKESRWAKPKELEDLEGYONTIVAG
			SLITKSNLHAMIKAEESSKOEECTTTSTAPVPTTEIPTTMSTMA
			AABAAAAVVAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
			EVTSIVATVVDNENTVTISTEEQAQLTSTPAIQDQSVEVSSNTG
			EETSKQBTVADFTPKKEEEESQPAKKTYTWNTKEEAKQAFKELL
1 .		1	KEKRYPSNASWEQAMKMIINDPRYSALAKLSEKKQAFNAYKVQT
1		ì	EKK
6334	. 17	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNONRSMEAHNILSER
1			GFSVRSFGTGTHVKLPGPAPDKPNVVDFKTTYDQMYNDLLRKDK
1			ELYTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYD
1			QVVEDLNSREQETCQPVHVVNVDIQDNHEEATLGAFLICELCQC
1			IQHTEDMENBIDELLQEFEEKSGRTFLHTVCFY
6335	82	529	AARARPGVLCCRLLGAALGDOSRVEMSYIPGOPVTAVVORVETH
			KLRQGENLILGFSIGGGIDODPSONPFSEDKTDKGIYVTRVSEG
			GPAEIAGLQIGDKIMQVMGWDMTMVTHDQARKRLTKRSEEVVRL
			LVTROSLOKAVOOSMLS
6336	2003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
			LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
i l			ADFWLTEKULIPKLFQVLAPRYKDQTGGYTRMLQIPNRSLDRAK
1			MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
1 1			NHSSHTAOTPGI
6337	76	524	EGIQMLSVQFDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
[ [			ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKI.T
			PAFENVMRAKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCO
L			TDYREGLMKEGYAPQVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
			GLRLALLLLGLGTPKSGVQGQEGLDFPEYEGVDRVINVNAKNY
i 1			KNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLED
			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
			ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
			DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLTLKLNEIDFYE
			AFMER PVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE
1			DDMDGIHIVAFAERADPDGFEFLETLKAVAQDNTENPDLSIIWI
			DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE
			DLPSAEELEDWLEDVLEGEINTEDDDDDDDD
6339	216	1813	NRCDRGGGQAERQAGQGCRTQGAGPGFGFGHSFFSQGAMKAFH
1 1			TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS
			VTESPQRVIITEDDRDETTVELEGQDENQEGDFEDADTQEGDTE
I			SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY
ı I			LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL
			VGDDCTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL
			KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
			DTKMVHFLTHYADKIESVHFSDOFSGPKINOREGOPLKLPDTKR
	Į.		TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE
	Į.		GKOKADKNRARVEENFLKLTHVOROEAAOSRREEKKRAEKERIM
			NEEDPEKORRLEEAALRREOKKLEKKOMKNKOIKVKAM
6340	2	583	BACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS
0340	*	203	SSSTSSSASRALPAODPPMEKALSMFSDDFGSFMRPHSEPLAF
			PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCOLPEDVDPTSVTSALREDGSLTIRARR
			HPHTEHVOOTPRTEIKI
6341	2	645	KMAVLSAPGLRGFRILGLRSSVGPAVOARGVHOSVATDGPSSTO
			DAT DEADAUA DEDCED COMMENT AT DOT TOWN DOCUMENTOR'S
	1		PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA CCAVEMMHMAAPRYDMDRFGVVFRASPROSDVMIVAGTLTNKMA

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
6342			VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGGGLWIGRPQSDMNNI
1		1	KPLEGVKILDLTRVLAGPFATMNI.GOLGAEVIKVERPGAGDDTR
1			TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
			DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
í		1	QRAGYDAVASAVEGLMHITGPEVACLSHIAANYLIGQKEAKRWG TAHGSIVPYQAFKTKDGYIVVGAGNNQQFATVCKILDLPELIDN
			SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
		i	PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
1			MSEARPPPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANFIWWGKQALKESQFTLSKCIDAV
			MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
			GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGOHT
1	i		BTLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
i			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
1			PQMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
1	!		IEIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK
			VSA
6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
			QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
1			QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
1			PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
J			VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
1			TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQFQLQQEARPQKQVQ POVQPQAHSQGPRQVQLQQEAEPLKQVQPQVOPQAHSQPPRQVQ
			LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPBOTHEO
			PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
			VGTQVSMBBIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI
			LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKOALOFFCY
			ICKAS CSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
			PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
!			DHFITVDAVGCFEGDEBEEEDDEDEEEIEVERELCKQVRSRDIS
1			REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
			SHCKSLGHFENLOKYKAAKNPSPITRPVSRRCAINARNALTALF
6345	2	2402	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
0345	4	3483	PRVKTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV
			HBLEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
	ļ		ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
			EQQATDQRSNIRDWVEMIKLHKQLVEKSNALSAMEGKFIQLQEK
			QRTLKISHDALMANGDELNMOLKBORLKCCSLEKOLHSMKFSER
			RIBBLQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
			QLKVQIAQLETALKSDLTDKTBILDRLKTERDQNEKLVQENREL
			QLQYLEQKQQLDELKKRIKLYNQENDINADELSEALLLIKAQKE
			QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
1 1			LIMOHKINKDYOMEVEAVTRKMENLQQDYKLKVEQYVHLLDIRA
			ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLBRG
			ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
	J		VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE
			TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
			RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
			SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
	i		DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
			DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH

SEQ Predicted Predicted end Amino acid segment containing signal mention

ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	boquonos	\=possible nucleotide insertion)
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
	1		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
			TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
			TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVLYVDK
			ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
1 1	ļ		GVAHVDLADMFOEGRDLIEONIDVFDARADGEGIGKLRVTVEAL
1 1			HALOSVYKOYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPPSALTPSIWPQEIL
1 1			AKYTOKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
			QGTGMVAACLLLFLEREDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHNFLTAFASVV
			DIKLLERIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
1			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
1 1			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
l i			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
1 1			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
(			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL
i			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQTKC
i			BLRVLCCFAFSLSQDWELPAKRBAQQPLKBGVRDMLVKHHLFSW
í l			DVEG
6347	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
			QGTGMVAACHLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1 1	,		DIKLLLRIWDLFFYEGSRVLFQLTLGNLHLKEEELIQSENSASI
	į į		FNTLSDIPSOMEDAELLLGVAMRLAGSLTDVAVETORRKHLAYL
ı 1			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
1 1	l J		KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHKNYVACSRSH
			RRRAKALLDFERHODDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGT_CPALK
	ļ		ALFEHGLKKPSLLGGACHPWLFIEBAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
			ELRVLCCFAPSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6348	3	3679	AGAEKCFVTLLACPLAKQONKYKYEBCKDLIKSMLRNELOFKEE
-510		3073	KLAEQLKQAEBLROYKVLVHSOBRELTOLREKLREGRDASRSLN
, ,			EHLQALLTPDEPDKSOGODLOBOLAEGCRLAOHLVOKLSPENDN
.			DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
		j	ILPVPGPTSSATNVSNVVSAGPLSGEKAAINILEINEKLRPQLA
' 1	Į.		
' I			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN EROFKERKLAROLKOAFELDOVKVLVHSORDELTOLDEKLDEGD
			ERQFKEBKLABQLKQABELRQYKVLVHSQBRELTQLREKLRBGR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valinc,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	eedneuce		\=possible nucleotide insertion)
1			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
1			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
1			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
1			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
1			BLLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRE:LEVVEPEVLQD
1	1		SLDRCYSTPSSCLEQPDSCQPYGSSFYALREKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGC_ELTDSCQPYRSAFYILEQQRVGLAV
			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
i			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
	i		PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
1	!		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
1 .			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVONRFFTLTVTSLHLVFQMGVIFPQ
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
		,	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEEGAITCS
1			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
			ERQFKEEKLAEQLKQABELRQYKVLVHSQERELTQLREKLREGR
			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
1 1	i		LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEBKEVPEDSLE
	J		ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
1			CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCFRLSR
į l			BLLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1			QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD
1			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
1 /			KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCFRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQAVGLAV
1			DMDBIEKYQEVEBDQDPSCPRLSGELLDBKEPEVLQESLDRCYS
1			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
1 1			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
1 1			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
1 1			VGFSLDVGEIEKKGKGKKRRGRRSKKBRRRGRKEGEEDONPPCP
1 1	1		RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
6350	3		SFEREHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6350	3	3679	AGABKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
1			KLABQLKQABELRQYKVLVHSQERELTQLREKLREGRDASRSLN
ı I			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
1 1		j	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
1 1		ļ	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
1 1	1	J	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEBCKDLIKFMLRN
1 1			ERQFKBEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
1 1			DASRSINEHLQALLTPDEPDKSQGQDLCEQLAEGCRLAQHLVQK
			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKABEKEVPEDSLE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K≈Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valing,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTKITFEEDXVDSTLIGSSSHVEW
	i e		EDAVHI I PENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDOVK
1			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
1			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGOPYSSAVYSLEE
ì	l		QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDERG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQORVGLAV
1			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLOESLDRCYS
1	1		TPSGCLELTDSCQFYRSAFYILEQQRVGLAVDMDEIEKYOEVEE
	i .		DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDOEEEEDOGPPCPRLSRRL
			LEVVEPEVLQDSLDRCYSTPSSCLEQFDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6351	1291	319	REARRITERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG
			RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP
			DSRHHSLALTSFKRQQBESFQEQSALAABARETRRQELLEKITE
			GQAAKKQKLEQASGASSSQEAGSSQAAKEDETSDGCASGEOERA
]			GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS
	,		KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD
			PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ
6352			PDGKVVYTSLQWASLQ
0352	235	923	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
1			AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG
			LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE
			PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
			TRRELABNLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
6353	65	600	DDCVYIVVD
0333	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
			VNTDDVNAI ILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
I			FLHHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS
			PLEEEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE
6354	965	510	DLSHVQPGSPAINGRSQTDDEEMTGE
0554	303	210	PSLRPMEPTRUCPLEGGAFSAILPMGAIDVSDLRPVPDNQEVFC
1			HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE
			SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA
6355	158	1662	LLRLPQYQTDLLLTFNQPP
0555	158	1062	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
]	Í	J	WDGKVSETKKKIKSILPGRSCDLLQDTSHLPPBHSDVVIVGGGV
	1		LGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ
1			QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
1			LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
1 1			ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
	1		SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
			WSAQIAALAGVGEGPPGTLQGTKLPVEPRXRYVYVWHCPQGPGL
i i	i i		ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD
			FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
			PLVVNMYFATGFSGHGLQCAPGIGRAVAEMVLKGRFQTIDLSPF
6356	354	633	LFTRFYLGEKIQENNII
****	234	633	TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEEEEEIEAREV
		1	ADSYAQNAKVIEKQLERKGMSKRRLQELAELEAKKAKMKGTLID NOFK
			MAK V

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide /	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H-Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
!	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\mpossible nucleotide insertion)
6357	2	915	GLIRNMALLVRVLRNOTSISOWVPVCSRLIPVSPTOGOGDRALS
			RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
		1	QPVEEKVGAFTKIIBAMGFTGPLKYSKWKIKIAALRMYTSCVEK
		1	TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEGRSGKYM
		}	CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNEFYAAILGY
1			DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL
			DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
			AISKTAVAPIBRVKLLLQVQHASKQIAADKQYKGIVDCZVRIPK
			EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTE
			REFRGLGDCLVKITKSDGIRGLYOGFSVSVOGIIIYRAAYFGVY
1			DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
	*		MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
1 1			GAFVLVLYDBLKKVI
6359	98	1086	VCRQEEEKMKEDCLPSSHVPISDSKSIOKSELLGLLKTVNCYHR
			GKSFOLRHREEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHI
1 1			PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDSS
1 1			GFLEEAEEAFQLMRTKSDASCMSQRRPKCRAFGEAQRIRRHRFS
1 1			INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV
			EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF
1 1			LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEBEEREIIKLT
6360	1	345	MKFQALRITMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN
1 1			PAQTAGNVFLKHGSELRIIPRDRVGSC
6361	615	158	RPGLGOLOHCALAPOAGNRRCRFHGRLHALTRSTHRGKPMSIMO
			FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
			APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIOAGDALMLPA
1			NSTGIWDIQETVRKTYVLIL
6362	350	1576	TIMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF
1 1			GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG
1 1			ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF
1 1			LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW
1 1			PFLLYMLVEIILFCLLLYFYKEKNAMNIVVILLLVALLGSMTVV
			TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ
			ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
1			ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMQNWHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMOEEHGSRSASG
			VPYRVLEHTKKE
6363	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG
1	~~	****	DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
			RYPMEHGIVKDWNDMERIWQYVYSKDQLOTFSEEHPVLLTEAPL
!			NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
1			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
			TIBIGPSRFRAPELLFRFDLIGEESEGIHEVLVFAIQKSDMDLR
1			RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
			RLYSTWIGGSILASLOTFKKMWVSKKEYERDGARSIHRKTF
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG
			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
1			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
1			NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPOKDETLETEKAOYYLPDGS
1			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

Deginning   Incleotide   Iocation   Iocati	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
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6369 1 1745 AGCCRDTRPPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMPQDSVAPEDVAVSFTQEEWALLDPSQKNLYRDVMQET				DQFVCGETVPAPSANKELVKC
PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET	6369	1	1745	AGCCRDTREPTPRGPGSLCHNFCRSAACTVTRTTHGGDFTDTGT
14Shard Caramana Cara			1	
	1			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHOG
ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD	1 1			PCFNOTADDMINUVET.DCTTDCTCCUCCQUCGCUCCC
	j			
TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY	1 1		1	
DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL	1			
IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHIGVNADECKE	1 1			
CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM			1	
THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA	1			
FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
EKPHECKBCGKVFKYFSSLRIHERTHIGEKPHECKQCGKAFRYF				
1				

SEQ	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nuclcotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
J	residue of	amino acid	S-Serine, T-Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	Dequence		SSLHIHBRTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY
			ECKHOGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE
	l		HERTHTINR
6370	1711	329	FVLSBQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
0370	1 *****	323	ALVGGLRPVTMTTPANAONASKTWELSLYELHRTPGEAIMDGTE
		i	IAVSPRSLHSELMCPICLDMLKGTMTTKECLHRFCSDCIVTALR
			SGNKSCPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHQD
			RVLIRLSRLHNQQALSSSIEEGLRNQAMERAQRVRRPIPGSDOT
			TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
			SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGGPSPPGAPS
		l	PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
		l	LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGGGGGGGGGG
		l	DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
			KFWKVSRPLELCYAPTKDPK
5371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
			LHNNNFENALCRESKEYLECRMERKLMLCEPLEKLGFGDLTSG
1		ĺ	KSEAKK
6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLOPVVMCVMKH
			LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
			LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
			VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
			BICTVDPCHKFTWCLDACIRERFVDSKRARBLOGFLDGVKKGOR
1			QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL
i I			LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
í !			DYTFNVDQKLPAREKAPVSYPNTLPESFTKFLOEORMACKVGLY
1 1			YVLHITKQRNKNALLRLLPGLVETFGDLAFGDIFLHLLTGNLAL
			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
			APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
1			QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
			DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA
			WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
			VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD
			GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
6374	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
			CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
			HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
	J		CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
			DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
			SGCHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
! I			IEQSVNEKIRDRLPVNVRRLSLDDPEVEQVSGRGLPDDHAGPIR
			VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
			SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL
l l			QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII
	1		ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL
6000			EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
	I		CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
	Ì		PPGRACSNPSFLRFQ=DFYQVYFLALAADWLQAPYLYKLYQHYY
			FLEGQIAILYVOGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY
			SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER
			HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP
			FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
			FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA
			FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i i	sequence	-	\=possible nucleotide insertion)
			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
			VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTD:DHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKOEGRO
1			QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
			NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAOGVKCADC
1			GLNVHKQCSKMVPNDCKFDLKHVKKVYSCDLTTLVKAHTTKRPM
1			VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
1			ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD
			PDEQLETIHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
6377			ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEDILF
6377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKQRRTFE
	İ		QRVEDVRLIREQHPTKIPVIIERYKGBKQLPVLCKTKFLVPDHV
1			NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE
6378	686	191	KDEDGFLYMVYASQETFGMKLSV
0370	000	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
			DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
			WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	PRACEDERONAL PROPERTY OF THE P
		370	ERAGSPSPSRAALRRCAPORSQAPRWPDRAACRRSFQGSQGRAY LFNSVVNVGCGPABERVLLTGLHAVADIYCENCKTTLGWKYEHA
			PESSQKYKBGKYIIBLAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
			GVDEPLSETGFKQAAAAGIFLNNVKPTHAFSSDLMRTKQTMHGI
1	1		LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
			CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADCKEQFSQGS
			PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
			MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
	l l		REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
			LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
1 1	1		YLASCVQYRLVVRDVNTLQILQLYTCLDQIQH:EWSADSLFILC
1			AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT
1			TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
1 1			RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVND
1			TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
			SYDGKVRILNHVTWKMITEFGHPAAINJPKIVVYKEAEKSPOLG
1 1			LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP
1			KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL
1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGBGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	2	1062	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
"	-		KHHVLETEKTPKDWVRQHRKEEKMKSHKLBEEFEWLKKSEVLYY
1			TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL
	I		LENLTSRYEVPCVLDLKMGTRQHGDDASE3KAANQIRKCQQSTS
1 1	l		AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF
1 1			HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
1 1			KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
			IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG
		1	В
6383	3159	1061	SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK
1 1	1		GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP
		1	AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
] ]			PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
1 1		1	SSSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
1			GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVBQKVQSLQA
			TFGTFESILRSSOHKODLTEKAVKQGESEVSRISEVLQKLQNEI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIA:F
Į.			TEVOKRSOKEINDMKAKVASLEESEGNKODLKALKEAVKEIGTS
1		ł	AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
	1		TERLALQALTEKLLRSBESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
			ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSL
1			GETQLVLYGDVEBLKRSVGBLPSTVESLQKVQKQVHTLLSQDQA
			QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
6384	738	1904	SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
0504	,30	1304	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGO
!			NPNATFGEVSQIVASMNDSLGEEQKQVYKRKTEAAKKEYLKALA
i			AYRASLVSKAAABSABAQTIRSVQQTLASTNLTSSLLLNTPLSQ
	J	ļ	HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQ
			QCQMQQMQQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQOH
1			LOQUINOCOLOCOLOCRECECCECHMONOSOPSPROMSPVASOI
			TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
1			LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
			ALEEVPLEVLRORESKWLDMLNNWDKWMAKKHKKIRLRCOKGIP
ł			PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
1			LHRQFPFHEMFVSRGGHGQQDLFRV:KAYTLYRPEEGYCQAQAP
			IAAVLIMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVL
1 .			RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER LRSLSPKIMQBAFLVQEVVELPVTERQIEREHLIOLRRWOETRG
			ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
			KAKPKPPKQAQKBQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
			PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
			RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
			PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
			PEAGDSRVHNSTOKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
	ļ j		KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
1			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6388			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
0300	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
1			KQBLAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQX
1			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1 1			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	ARPGDRMAGHRLVLVLGDLHIPHRCNSLPAKPKKLLVPGKIQHI
			LCIGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
1	·		QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
		1	EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
1	İ		LIGDDVKVERIEYKKP
6390	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
			LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
L			SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTORKLKA
1			MSLLGSRNQLARAVLNPNPMDFCTKDLLTCTSERIIAYLRDFNE
			DOKKATETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
1 1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence		\-possible nucleotide insertion)
			LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF
			KEKCKDKKNPLGNCGDINLVRLGPEKSINSEVLKFSLDSQUNHR
		1	MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGREIQRQEL
1 i		ĺ	DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS
1 1			TSGGLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
1 1		ľ	KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN
1 1			MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
1 1			SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD
1 1			KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA
1 1			FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
1 1			ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK
1			LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGFAKTSVAASL
1			YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG
			IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQOPAAVVAA
1 1			LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
1			GEQEKCGSETHHTRRNSRWDKRTLEQEDSSSKKRKLL
6392	972	186	GRTGVDLASSMAHRLQIRLLTWDVKDTLLRLRHPLGRAYATKAR
	272	200	AHGLEVEPSALEGGFRQAYRAQSHSFPNYGLSHGLTSRQWWLDV
1 1			VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPCTWQVLDGAEDTLR
1 1			ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
1 1			KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL
			VVGPQALDFVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT
		/50	NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV
			LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ
1 1			ELPAPLLDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME
1 1			IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
1 1			EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
1 1			LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
1 !			PTHLIQNKAIIARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
1 1			IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD
1 1			TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARRPAAMATVMAATAAERAVLEEEFRWLLHDEVHA
			VI.KQI.QDILKEASI.RFTLPGSGTEGPAKQENFILGSCGTDQVKG
1 1			VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKOWKLQQIQDAR
1 1			NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLT
1 1			TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
1 1			LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC
1 1			VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYMSYRPF
6395	13	658	PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPTETSNPGSSVM
			ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP
			PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ
1		J	DLLEEASSRDMQMGPGLFLRMQLVPS IEERETPLTREDRPALQ3
	ł	ļ	PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANILSSPSKRGOKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
1 1	- 1	i	IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI
1			SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
	1		INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
	1		IGTCAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
	1		GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEOFGWFIAD
	Į.	J	PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
			IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
			TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
		1	MKYCKDGTYIM
6397	391	122	GAGGVGRFEATRAPARMTEVVCNDRTGKKVRVKCNTDDTTGDLF
6397	391	122	GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY